

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 8, 2006, 19:37:09 ; Search time 246 Seconds  
(without alignments)  
897.684 Million cell updates/sec

Title: US-10-063-595-88

Perfect score: 1747

Sequence: 1 MNQLSFLFLIATTRGWSSTD.....HVGYSRRITEAAVLLFYR 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1747	100.0	313	2 Q51WS5_HUMAN	Q51ws5 homo sapien
2	1738	99.5	313	1 ITLN1_HUMAN	Q8wwa0 homo sapien
3	1738	99.5	313	2 Q5VVI4_HUMAN	Q5vvi4 homo sapien
4	1733	99.2	313	2 Q5VWS4_HUMAN	Q5iws4 homo sapien
5	1449.5	83.0	325	1 ITLN2_HUMAN	Q8wwi7 homo sapien
6	1449.5	83.0	325	2 Q5VVI0_HUMAN	Q5vvi0 homo sapien
7	1427	81.7	313	1 ITL1A_MOUSE	O88310 mus musculus
8	1427	81.7	313	1 Q51WS3_MOUSE	Q5iws3 mus musculus
9	1391	79.6	313	1 ITL1B_MOUSE	O80za0 mus musculus
10	1129	64.6	339	2 Q6P7Y6_XENTR	Q6p7y6 xenopus tro
11	1105.5	63.3	338	2 Q8JJD0_XENLA	Q8jjd0 xenopus lae
12	1103	63.1	342	2 Q800K0_XENLA	Q800k0 xenopus lae
13	1095	62.7	339	2 Q5PPM0_XENLA	Q5ppm0 xenopus lae
14	1080	61.8	315	2 Q8JJC9_XENLA	Q8jjc9 xenopus lae
15	1049.5	60.1	313	2 Q61719_XENLA	Q91719 xenopus lae
16	1049	60.0	285	2 Q6GR52_XENLA	Q6gr52 xenopus lae
17	1047.5	60.0	320	2 Q5U4L0_XENLA	Q5u4l0 xenopus lae
18	1044.5	59.8	321	2 P79957_XENLA	P79957 xenopus lae
19	1034	59.2	321	2 Q6GP37_XENLA	Q6gp37 xenopus lae
20	1025	58.7	320	2 Q8AWX0_XENTR	Q8awx0 xenopus tro
21	892	51.1	333	2 Q98TC9_LAMJA	Q98tc9 lampetra ja
22	873	50.0	318	2 Q4U121_CTEID	Q4u122 ctenopharyn
23	870	49.8	318	2 Q4U121_CTEID	Q4u121 ctenopharyn
24	820.5	47.0	320	2 Q4W8M6_LAMJA	Q4w8m6 lampetra ja
25	755	43.2	256	2 Q6DEN7_XENTR	Q6den7 xenopus tro
26	347.5	19.9	579	2 Q69HM9_CIOIN	Q69hm9 ciona intes
27	293.5	16.8	121	2 Q9DPE0_ONCMY	Q9dfe0 oncorhynch
28	129.5	7.4	282	1 F1BA_PARPA	P19477 parastichop
29	125.5	7.2	475	2 Q6MK33_BDEBA	Q6mk33 bdellovibri
30	125	7.2	488	2 Q6MK34_BDEBA	Q6mk34 bdellovibri
31	119.5	6.8	485	2 Q6NYE1_BRARE	Q6nye1 brachydanio

32	115.5	6.6	457	2 Q5XK91_XENLA	Q5xk91 xenopus lae
33	111.5	6.4	1946	2 Q4S290_TETNG	Q4s290 tetraodon
34	110.5	6.3	451	2 Q5TYU3_BRARE	Q5tyu3 brachydanio
35	110.5	6.3	525	2 Q4LES0_BRARE	Q4les0 brachydanio
36	110.5	6.3	1296	2 Q70HX0_MOUSE	Q70hx0 mus musculus
37	109.5	6.3	189	2 Q5HX51_CAMJR	Q5hx51 campylobact
38	109.5	6.3	1560	1 TENN_MOUSE	Q80r71 mus musculus
39	109	6.2	306	2 Q5EAM5_XENTR	Q5eam5 xenopus tro
40	109	6.2	491	1 F1BB_HUMAN	P02r75 homo sapien
41	109	6.2	491	2 Q5R535_PONPY	Q5r535 pongo pygma
42	107.5	6.2	1243	2 Q9UVC1_CLAFU	Q9uvc1 cladospriu
43	107	6.1	310	2 Q7QHK2_ANOGA	Q7qhk2 anopheles g
44	106.5	6.1	246	2 Q9V7U5_DROME	Q9v7u5 drosophila
45	106.5	6.1	318	2 Q5BKK1_XENTR	Q5bkk1 xenopus tro
46	106.5	6.1	649	2 Q7VY64_BORPE	Q7vy64 bordetella
47	106.5	6.1	649	2 Q7W912_BORPA	Q7w912 bordetella
48	106.5	6.1	649	2 Q7WKP7_BORBR	Q7wkp7 bordetella
49	106	6.1	1294	1 TENN_HUMAN	Q9uqp3 homo sapien
50	106	6.1	1299	2 Q5R360_HUMAN	Q5r360 homo sapien
51	105.5	6.0	189	2 Q9PJ12_CAMJE	Q9pj12 campylobact
52	105.5	6.0	269	2 O8BL54_MOUSE	O8bl54 mus musculus
53	105.5	6.0	616	2 O16770_CAEEL	O16770 caenorhabdi
54	105	6.0	434	2 O52730_9BACI	O52730 bacillus sp
55	104.5	6.0	270	2 Q91332_RANSY	Q91332 rana sylvat
56	104.5	6.0	426	2 Q5XMK6_9HEPC	Q5xm6 hepatitis c
57	104.5	6.0	427	2 Q4SEZ4_TETNG	Q4sez4 tetraodon n
58	103.5	5.9	190	2 Q4HFP0_CAMCO	Q4hfp0 campylobact
59	103.5	5.9	426	2 Q5XMY0_9HEPC	Q5xmy0 hepatitis c
60	103.5	5.9	426	2 Q5XMY3_9HEPC	Q5xmy3 hepatitis c
61	103.5	5.9	426	2 Q5XMY5_9HEPC	Q5xmy5 hepatitis c
62	103.5	5.9	1917	2 Q51ED6_ENTHI	Q51ed6 entamoeba h
63	103.5	5.9	2301	2 Q95Z81_9UROC	Q95z81 oikopleura
64	103	5.9	337	2 Q9BE00_MACFA	Q9be00 macaca fasc
65	103	5.9	429	2 Q8TF00_METAC	Q8tf00 methanosarc
66	103	5.9	470	2 Q4S2B3_TETNG	Q4s2b3 tetraodon n
67	102.5	5.9	426	2 Q5XMY4_9HEPC	Q5xmy4 hepatitis c
68	102.5	5.9	457	2 Q6AX44_XENLA	Q6ax44 xenopus lae
69	102.5	5.9	592	2 Q7UJX1_RHOBA	Q7ujx1 rhodopirell
70	102	5.8	481	1 F1BB_MOUSE	O8x0e8 mus musculus
71	102	5.8	481	2 Q5R6W8_PONPY	Q5r6w8 pongo pygma
72	102	5.8	550	2 Q4FDS5_GSOSL	Q4fds5 geobacter s
73	101.5	5.8	269	2 Q8BJE7_MOUSE	Q8bj7 mus musculus
74	101.5	5.8	280	2 Q9J526_CHICK	Q9j526 gallus gall
75	101.5	5.8	399	2 Q4WKU8_ASPFU	Q4wku8 aspergillus
76	101.5	5.8	426	2 Q5XMX8_9HEPC	Q5xm8 hepatitis c
77	101.5	5.8	426	2 Q5XMY1_9HEPC	Q5xmy1 hepatitis c
78	101.5	5.8	426	2 Q5XMY4_9HEPC	Q5xmy4 hepatitis c
79	101.5	5.8	459	2 Q6P9R8_MOUSE	Q6p9r8 mus musculus
80	101.5	5.8	680	2 Q8ED23_SHEON	Q8ed23 shewanella
81	101	5.8	363	2 Q9VF34_DROME	Q9vf34 drosophila
82	101	5.8	427	2 Q86H02_BIOGL	Q86h02 biomphalari
83	101	5.8	732	2 Q86H03_BIOGL	Q86h03 biomphalari
84	100.5	5.8	426	2 Q5XMY2_9HEPC	Q5xmy2 hepatitis c
85	100.5	5.8	426	2 Q5XMY8_9HEPC	Q5xmy8 hepatitis c
86	100.5	5.8	426	2 Q5XMY5_9HEPC	Q5xmy5 hepatitis c
87	100.5	5.8	426	2 Q5XMY6_9HEPC	Q5xmy6 hepatitis c
88	100.5	5.8	655	2 Q86H06_BIOGL	Q86h06 biomphalari
89	100	5.7	572	2 Q8B9F4_NPVRO	Q8b9f4 rachiplusia
90	100	5.7	796	2 Q6V2E1_ENTAS	Q6v2e1 enterobacte
91	100	5.7	2265	1 F1NC_BOVIN	P07589 bos taurus
92	99.5	5.7	318	2 Q5U490_XENLA	Q5u490 xenopus lae
93	99.5	5.7	318	2 Q7ZT74_XENLA	Q7zt74 xenopus lae
94	99.5	5.7	426	2 Q5XMX7_9HEPC	Q5xm7 hepatitis c
95	99.5	5.7	2752	2 Q61TES_CABER	Q61te9 caenorhabdi
96	99	5.7	274	2 Q57S28_SALTY	Q57s28 salmonella
97	99	5.7	274	2 Q8ZR67_SALTY	Q8zr67 salmonella
98	99	5.7	279	2 Q7YXMO_ORNMO	Q7yxmo ornithodora
99	99	5.7	308	2 Q5XG23_XENLA	Q5xg23 xenopus lae
100	99	5.7	308	2 Q7ZT75_XENLA	Q7zt75 xenopus lae
101	99	5.7	375	1 ANGP2_BOVIN	P12799 bos taurus
102	99	5.7	444	1 F1BG_BOVIN	Q9y5c1 homo sapien
103	99	5.7	460	1 ANGL3_HUMAN	Q9stax7 homo sapien
104	99	5.7	460	2 Q5TAX7_HUMAN	

105	99	5.7	466	2	Q4T9V4_TETNG	Q4t9v4 tetraodon n	178	93.5	5.4	1701	2	Q9V3E8_DROME	Q9v3e8 drosophila
106	99	5.7	479	1	FIBB_RAT	P14480 rattus norv	179	93	5.3	314	2	Q8VC25_MOUSE	Q8vc25 mus musculus
107	99	5.7	479	2	Q5I0E7_RAT	Q5i0p7 rattus norv	180	93	5.3	314	2	Q71KU9_MOUSE	Q71ku9 mus musculus
108	99	5.7	503	2	Q7TME5_RAT	Q7tme5 rattus norv	181	93	5.3	364	2	Q5B8S7_XENLA	Q5b8s7 aspergillus
109	99	5.7	796	1	DHG_ECOLI	P15877 escherichia	182	93	5.3	468	1	FIBB_BOVIN	P02676 bos taurus
110	99	5.7	796	2	Q8X946_RCO57	Q8x946 escherichia	183	93	5.3	536	2	Q7V8Q0_PROMM	Q7v8q0 prochloroc
111	98.5	5.6	802	2	Q8FL38_ECOL6	Q8fl38 escherichia	184	92.5	5.3	218	2	Q6UY50_HUMAN	Q6uy50 homo sapien
112	98.5	5.6	259	2	Q7QHK6_ANOGA	Q7qhk6 anopheles g	185	92.5	5.3	279	2	Q6JKK9_9DIPT	Q6jkk9 armigares s
113	98.5	5.6	426	2	Q5XMK5_9HEPC	Q5xmk5 hepatitis c	186	92.5	5.3	288	2	Q6UXM4_HUMAN	Q6uxm4 homo sapien
114	98.5	5.6	426	2	Q5XMK6_9HEPC	Q5xmk6 hepatitis c	187	92.5	5.3	299	1	FCN3_HUMAN	Q75636 homo sapien
115	98.5	5.6	426	2	Q5XMK7_9HEPC	Q5xmk7 hepatitis c	188	92.5	5.3	299	1	FCN3_HUMAN	Q75636 homo sapien
116	98.5	5.6	426	2	Q5XMK2_9HEPC	Q5xmk2 hepatitis c	189	92.5	5.3	348	2	Q4SF82_TETNG	Q4sf82 tetraodon n
117	98.5	5.6	462	2	Q6E7H1_PIG	Q6e7h1 sus scrofa	190	92.5	5.3	426	2	Q5XMR8_9HEPC	Q5xmr8 hepatitis c
118	98.5	5.6	652	2	Q4SIU0_TETNG	Q4siu0 tetraodon n	191	92.5	5.3	426	2	Q5XMT7_9HEPC	Q5xmt7 hepatitis c
119	98.5	5.6	725	2	Q9JUX3_NEIMB	Q9jux3 neisseria m	192	92.5	5.3	426	2	Q5XMK0_9HEPC	Q5xmk0 hepatitis c
120	98.5	5.6	777	2	Q7QHLU_ANOGA	Q7qhl0 anopheles g	193	92.5	5.3	426	2	Q5XMK3_9HEPC	Q5xmk3 hepatitis c
121	98.5	5.6	777	2	Q5R975_PONPY	Q5r975 pongo pygma	194	92.5	5.3	490	1	ANGL1_MOUSE	Q640p2 mus musculus
122	98	5.6	481	2	Q83SM2_SHIFL	Q83sm2 shigella fl	195	92.5	5.3	576	2	Q4KP46_9HEPC	Q4kp46 hepatitis c
123	98	5.6	776	2	Q7UDR6_SHIFL	Q7udr6 shigella fl	196	92.5	5.3	694	2	Q87TP9_VIBPA	Q87tp9 vibrio para
124	98	5.6	796	2	Q83SM2_SHIFL	Q83sm2 shigella fl	197	92.5	5.3	1077	2	Q977X0_METMA	Q977x0 methanosarc
125	97.5	5.6	324	2	Q95P99_HALRO	Q95p99 halocynthia	198	92.5	5.3	1077	2	Q977X1_METMA	Q977x1 methanosarc
126	97.5	5.6	426	2	Q5XMR7_9HEPC	Q5xmr7 hepatitis c	199	92.5	5.3	1095	2	Q8PX82_METMA	Q8px82 methanosarc
127	97.5	5.6	426	2	Q5XMR4_9HEPC	Q5xmr4 hepatitis c	200	92.5	5.3	1319	2	Q45599_CAREL	Q45599 caenorhabdi
128	97.5	5.6	426	2	Q5XMK9_9HEPC	Q5xmk9 hepatitis c	201	92.5	5.3	1324	2	Q4RJ05_TETNG	Q4rj05 tetraodon n
129	97.5	5.6	426	2	Q5XMY7_9HEPC	Q5xmy7 hepatitis c	202	92.5	5.3	1710	2	Q4FAL8_BRARE	Q4fai8 brachydanio
130	97.5	5.6	431	2	Q95IU3_MACFA	Q95iu3 macaca faec	203	92	5.3	314	2	Q5M8C6_RAT	Q5m8c6 rattus norv
131	97.5	5.6	496	1	ANGP2_PIG	Q9bdy7 sus scrofa	204	92	5.3	321	2	Q5M8W6_XENTR	Q5m8w6 xenopus tro
132	97.5	5.6	509	1	ANGP4_MOUSE	Q9wvh6 mus musculus	205	92	5.3	421	2	Q95UV8_BIOGL	Q95uv8 biophalari
133	97.5	5.6	627	2	Q60JUV5_CAEBR	Q60juv5 caenorhabdi	206	92	5.3	484	2	Q4RHE8_TETNG	Q4rhe8 tetraodon n
134	97	5.6	495	1	CROM_OCTDO	P30841 octopus dof	207	92	5.3	496	1	ANGP2_HUMAN	Q5123 homo sapien
135	96.5	5.5	318	2	Q7ZT72_XENLA	Q7zt72 xenopus lae	208	92	5.3	796	2	Q8Z9E0_SALTI	Q8z9e0 salmonella
136	96.5	5.5	426	2	Q5XMR6_9HEPC	Q5xmr6 hepatitis c	209	91.5	5.2	194	2	Q4HMZ3_CAMLA	Q4hmz3 campylobact
137	96.5	5.5	426	2	Q5XMR9_9HEPC	Q5xmr9 hepatitis c	210	91.5	5.2	280	2	Q6VFG6_ANOGA	Q6vfg6 anopheles g
138	96.5	5.5	426	2	Q5XMS0_9HEPC	Q5xms0 hepatitis c	211	91.5	5.2	321	2	Q4WYX7_ASFPU	Q4wyx7 aspergillus
139	96.5	5.5	426	2	Q5XMS2_9HEPC	Q5xms2 hepatitis c	212	91.5	5.2	426	2	Q5XND9_9HEPC	Q5xnd9 hepatitis c
140	96.5	5.5	426	2	Q6UXK6_HUMAN	Q6uxk6 homo sapien	213	91.5	5.2	619	1	CHIT_STRLI	P36909 streptomyce
141	96.5	5.5	461	2	Q8NS39_HUMAN	Q8ns39 homo sapien	214	91.5	5.2	1646	2	Q4PQJ3_9HEPC	Q4pqj3 hepatitis c
142	96.5	5.5	496	1	ANGP2_MOUSE	Q35608 mus musculus	215	91.5	5.2	1840	2	Q59IP3_PIG	Q59ip3 sus scrofa
143	96.5	5.5	3700	2	Q4KAE3_PSEF5	Q4kae3 pseudomonas	216	91	5.2	324	2	Q85PA0_HALRO	Q85pa0 halocynthia
144	96	5.5	1746	2	Q5G216_XANOR	Q5g216 xanthomonas	217	91	5.2	325	2	Q8D555_VIBUO	Q8d555 vibrio vuln
145	96	5.5	3010	2	Q91AU0_9HEPC	Q91au0 hepatitis c	218	91	5.2	464	2	Q9AZ86_9CAUD	Q9az86 lactobacill
146	95.5	5.5	380	2	Q6VFG8_ANOGA	Q6vfg8 anopheles g	219	91	5.2	493	1	ANGL2_MOUSE	Q9r045 mus musculus
147	95.5	5.5	338	2	Q4YH92_TETNG	Q4yh92 tetraodon n	220	91	5.2	493	2	Q9JJ03_RAT	Q9jj03 rattus norv
148	95.5	5.5	363	2	Q7QHI4_ANOGA	Q7qhi4 anopheles g	221	91	5.2	501	2	Q8BM09_MOUSE	Q8bm09 mus musculus
149	95.5	5.5	426	2	Q5XMS1_9HEPC	Q5xms1 hepatitis c	222	91	5.2	626	2	Q9H019_HUMAN	Q9h019 homo sapien
150	95.5	5.5	450	1	UTH1_YEAST	P36135 saccharomyc	223	91	5.2	626	2	Q96M82_HUMAN	Q96m82 homo sapien
151	95.5	5.5	463	1	FIBB_CHICK	Q02020 gallus gall	224	91	5.2	642	2	Q61EH5_CAEBR	Q61eh5 caenorhabdi
152	95.5	5.5	477	1	FIBB_PETMA	P02678 petromyzon	225	91	5.2	733	2	Q5V334_HALMA	Q5v334 haloarcula
153	95.5	5.5	502	2	Q4RHE0_TETNG	Q4rnp0 tetraodon n	226	91	5.2	796	2	Q5NRA2_ZYMMO	Q5nra2 zymomonas m
154	95	5.4	576	2	Q4KP41_9HEPC	Q4kp41 hepatitis c	227	91	5.2	836	2	Q8EF34_SHEON	Q8ef34 shewanella
155	95	5.4	725	2	Q9JW26_NEIMA	Q9jw26 neisseria m	228	91	5.2	1778	2	Q5SP04_CRYNE	Q5sp04 cryptococcu
156	94.5	5.4	347	2	Q5K9X7_CRYNE	Q5k9x7 cryptococcu	229	91	5.2	3010	2	Q9QIX1_9HEPC	Q9qix1 hepatitis c
157	94.5	5.4	372	2	Q55JM4_CRYNE	Q55jm4 cryptococcu	230	90.5	5.2	220	2	Q8T8A2_CIOSA	Q8t8a2 ciona savig
158	94.5	5.4	413	2	Q18544_BIOGL	Q18544 biophalari	231	90.5	5.2	244	2	Q9HBP3_HUMAN	Q9hbp3 homo sapien
159	94.5	5.4	614	2	Q90484_BRARE	Q90484 brachydanio	232	90.5	5.2	279	2	Q5YD77_9ARAC	Q5ydt77 loxosceles
160	94.5	5.4	649	2	Q97U94_SULSO	Q97u94 sulfolobus	233	90.5	5.2	296	2	Q7OHN9_ANOGA	Q7ohn9 anopheles g
161	94.5	5.4	685	2	Q6D2W3_ERWCT	Q6d2w3 erwinia car	234	90.5	5.2	426	2	Q5XN72_9HEPC	Q5xn72 hepatitis c
162	94.5	5.4	1203	2	Q86KZ0_DICTDI	Q86kz0 dictyosteli	235	90.5	5.2	426	2	Q5XN83_9HEPC	Q5xn83 hepatitis c
163	94	5.4	325	2	Q87FH2_VIBPA	Q87fh2 vibrio para	236	90.5	5.2	439	2	Q5U565_XENLA	Q5u565 xenopus lae
164	94	5.4	338	2	Q5XJQ0_BRARE	Q5xjq0 brachydanio	237	90.5	5.2	576	2	Q4KP50_9HEPC	Q4kp50 hepatitis c
165	94	5.4	453	2	Q8CED0_MOUSE	Q8ced0 mus musculus	238	90.5	5.2	876	2	Q9LAJ2_CLOCL	Q9laj2 clostridium
166	94	5.4	484	2	Q5JH8E_PYRKO	Q5jhs5 pyrococcus	239	90.5	5.2	1644	2	Q4PQJ6_9HEPC	Q4pqj6 hepatitis c
167	94	5.4	511	2	Q4FKK6_9TRYP	Q4fkk6 trypanosoma	240	90.5	5.2	1899	2	Q54JX1_DICDI	Q54jx1 dictyosteli
168	94	5.4	1018	2	Q8YK71_ANASP	Q8yk71 anabaena sp	241	90.5	5.2	2742	2	Q5ULI6_9HEPC	Q5uli6 hepatitis c
169	94	5.4	1778	2	Q5KEF3_CRYNE	Q5kef3 cryptococcu	242	90.5	5.2	2742	2	Q5ULI6_9HEPC	Q5uli6 hepatitis c
170	93.5	5.4	413	2	Q7VK58_HELHP	Q7vk58 helicobacte	243	90.5	5.2	191	2	Q9EW89_STROI	Q9ew89 streptomyce
171	93.5	5.4	426	2	Q5XMT5_9HEPC	Q5xmt5 hepatitis c	244	90	5.2	198	2	Q8YSY3_DROME	Q8ysy3 drosophila
172	93.5	5.4	426	2	Q5XMT6_9HEPC	Q5xmt6 hepatitis c	245	90	5.2	325	2	Q7MBZ2_VIBVY	Q7mbz2 vibrio vuln
173	93.5	5.4	426	2	Q5XMT9_9HEPC	Q5xmt9 hepatitis c	246	90	5.2	372	2	Q18545_BIOGL	Q18545 biophalari
174	93.5	5.4	426	2	Q5XN45_9HEPC	Q5xn45 hepatitis c	247	90	5.2	385	2	Q95UV8_BIOGL	Q95uv8 biophalari
175	93.5	5.4	426	2	Q5XN48_9HEPC	Q5xn48 brachydanio	248	90	5.2	426	2	Q5XNJ8_9HEPC	Q5xnj8 hepatitis c
176	93.5	5.4	489	2	Q5KQT8_BRARE	Q5kqt8 brachydanio	249	90	5.2	510	2	Q5KQT9_BRARE	Q5kqt9 brachydanio
177	93.5	5.4	551	1	AMYE_THETU	P19584 thermoanaer	250	90	5.2				

251	90	5.2	557	1	EIL5_ARATH	Q9fjq5 arabidopsis	324	88	5.0	964	2	Q41386_SPIOL	Q41386 spinacia ol
252	90	5.2	648	2	Q9C1C6 COCCA	Q9c1c6 cochliobolu	325	88	5.0	1095	2	Q6C4Q2_YARLI	Q6c4q2 yarrowia li
253	90	5.2	660	2	Q8NCT0 HUMAN	Q8ncto homo sapien	326	88	5.0	1914	2	Q91008_CHICK	Q91008 gallus gall
254	90	5.2	2201	1	TENA_HUMAN	P24821 homo sapien	327	88	5.0	2082	2	Q9ACP4_STRCO	Q9acp4 streptomyce
255	90	5.2	2201	2	Q577S3_HUMAN	Q5t7s3 homo sapien	328	88	5.0	4833	2	Q4RNG0_TETNG	Q4rng0 tetraodon n
256	90	5.2	2233	2	Q577S3_HUMAN	Q4le33 homo sapien	329	87.5	5.0	321	2	Q4WEA8_ASPPU	Q4wea8 aspergillus
257	89.5	5.1	185	2	Q4HOY7_CANUP	Q4hyo7 campylobact	330	87.5	5.0	342	2	Q6ZM91_BRARE	Q6zm91 brachydanio
258	89.5	5.1	199	2	Q4JIY7_CITSI	Q4jiy7 citrus sine	331	87.5	5.0	410	2	O97645_MACRU	O97645 macropus ru
259	89.5	5.1	426	2	Q5XMY9_HEPC	Q5xmy9 hepatitis c	332	87.5	5.0	426	2	Q5XMU5_HEPC	Q5xmu5 hepatitis c
260	89.5	5.1	437	2	Q68FY3_RAT	Q68fy3 rattus norv	333	87.5	5.0	426	2	Q5XNE2_9HEPC	Q5xne2 hepatitis c
261	89.5	5.1	486	2	Q505I1_XENTR	Q505i1 xenopus tro	334	87.5	5.0	503	1	ANGP4_HUMAN	Q9y264 homo sapien
262	89.5	5.1	576	2	Q4KP43_9HEPC	Q4kp43 hepatitis c	335	87.5	5.0	503	2	Q5TFP4_HUMAN	Q5tfp4 homo sapien
263	89.5	5.1	576	2	Q4KP47_9HEPC	Q4kp47 hepatitis c	336	87.5	5.0	558	2	Q8TI42_METAC	Q8ti42 methanosarc
264	89.5	5.1	611	2	Q68002_BRAJE	Q68002 brachyrhizob	337	87.5	5.0	576	2	Q4KP51_9HEPC	Q4kp51 hepatitis c
265	89.5	5.1	719	2	Q8VLY7_TREDE	Q8vly7 treponema d	338	87.5	5.0	576	2	Q4KP52_9HEPC	Q4kp52 hepatitis c
266	89.5	5.1	791	1	ADMLA_MOUSE	Q60813 mus musculus	339	87.5	5.0	718	2	Q8RVT2_ORYSA	Q8rvt2 oryza sativ
267	89.5	5.1	1046	1	Q5AQUO_EMENI	Q5aquo emericillus	340	87.5	5.0	725	2	Q88QF9_PSBPK	Q88qf9 pseudomonas
268	89.5	5.1	1054	1	TRGA_EMENI	P78617 emericella	341	87.5	5.0	839	2	Q04207_ARATH	Q04207 arabidopsis
269	89.5	5.1	1532	2	Q90994_CHICK	Q90994 gallus gall	342	87.5	5.0	913	1	Y1217_HAEIN	P45114 haemophilus
270	89.5	5.1	1646	2	Q4PQU5_9HEPC	Q4pqu5 hepatitis c	343	87.5	5.0	943	2	Q4IM19_GIBZE	Q4im19 gibberella
271	89.5	5.1	1714	2	Q90995_CHICK	Q90995 gallus gall	344	87.5	5.0	1053	2	Q5B665_VIBP1	Q5b665 vibrio fisc
272	89.5	5.1	1808	1	TENA_CHICK	P10039 gallus gall	345	87.5	5.0	1419	2	Q6D375_ERWCT	Q6d375 erwinia car
273	89.5	5.1	1810	1	Q90824_CHICK	Q90824 gallus gall	346	87.5	5.0	1472	2	Q9U5A8_BOMMO	Q9u5a8 bombyx mori
274	89.5	5.1	2477	1	FINC_MOUSE	P11276 mus musculus	347	87.5	5.0	1561	2	Q675X9_9UROC	Q675x9 oikopleura
275	89	5.1	198	2	Q86FL1_SUBDO	Q86fl1 suberites d	348	87.5	5.0	1644	2	Q4PQU8_9HEPC	Q4pqu8 hepatitis c
276	89	5.1	266	2	Q4NV83_9DELT	Q4nv83 anaeromyxob	349	87.5	5.0	1646	2	Q4PQU4_9HEPC	Q4pqu4 hepatitis c
277	89	5.1	457	1	ANGL6_MOUSE	Q8r026 mus musculus	350	87.5	5.0	1646	2	Q4PQU0_9HEPC	Q4pqu0 hepatitis c
278	89	5.1	470	1	ANGL6_HUMAN	Q8ni99 homo sapien	351	87.5	5.0	1976	2	Q5D869_ARATH	Q5d869 arabidopsis
279	89	5.1	506	2	Q5LFD3_BACFN	Q5lfd3 bacteroides	352	87.5	5.0	2370	2	Q8ZRE3_STRAW	Q8zre3 streptomyce
280	89	5.1	567	2	Q5LUB90_BACFN	Q5lub90 bacteroides	353	87.5	5.0	2817	2	Q97K42_CLOAB	Q97k42 clostridium
281	89	5.1	567	2	Q64RN7_BACFR	Q64rn7 bacteroides	354	87	5.0	236	2	Q8N2J9_HUMAN	Q8n2j9 homo sapien
282	89	5.1	611	2	Q5BB43_EMENI	Q5bb43 aspergillus	355	87	5.0	255	1	MPAP4_BOVIN	P55918 bos taurus
283	89	5.1	649	2	Q4RR18_TETNG	Q4rr18 tetraodon n	356	87	5.0	361	1	GLNA_PANAR	Q04831 panulirus a
284	89	5.1	782	1	HMPB_DROME	P31264 drosophila	357	87	5.0	426	2	Q5XNJ4_9HEPC	Q5xnj4 hepatitis c
285	89	5.1	798	2	Q4JFI5_DROME	Q4jfi5 drosophila	358	87	5.0	426	2	Q5XNJ9_9HEPC	Q5xnj9 hepatitis c
286	89	5.1	865	2	Q7Q7V8_ANOGA	Q7q7v8 anopheles g	359	87	5.0	426	2	Q5XNK2_9HEPC	Q5xnk2 hepatitis c
287	89	5.1	923	2	Q4RVC9_TETNG	Q4rvc9 tetraodon n	360	87	5.0	493	1	ANGL2_HUMAN	Q9uk99 homo sapien
288	89	5.1	997	2	Q9Z4I1_9BACI	Q9z4i1 bacillus sp	361	87	5.0	493	2	Q5JT58_HUMAN	Q5jt58 homo sapien
289	89	5.1	1804	2	Q9P9A9_9EURY	Q9p9a9 uncultured	362	87	5.0	536	2	Q7ZXXQ2_XENLA	Q7zxxq2 xenopus lae
290	89	5.1	2351	2	Q23372_ARATH	O23372 arabidopsis	363	87	5.0	545	2	Q9CF03_LACLA	Q9cf03 lactococcus
291	89	5.1	3010	2	Q9QIX3_9HEPC	Q9qix3 hepatitis c	364	87	5.0	563	2	Q4TF93_TETNG	Q4tf93 tetraodon n
292	88.5	5.1	426	2	Q5XMR2_9HEPC	Q5xmr2 hepatitis c	365	87	5.0	585	2	Q8NFM1_HUMAN	Q8nfm1 homo sapien
293	88.5	5.1	426	2	Q5XMR3_9HEPC	Q5xmr3 hepatitis c	366	87	5.0	646	2	Q08347_YEAST	Q08347 saccharomyc
294	88.5	5.1	426	2	Q5XMR4_9HEPC	Q5xmr4 hepatitis c	367	87	5.0	776	2	Q764N8_9ASCO	Q764n8 geotrichum
295	88.5	5.1	426	2	Q5XMR5_9HEPC	Q5xmr5 hepatitis c	368	87	5.0	806	2	Q5H2N7_XANOR	Q5h2n7 xanthomonas
296	88.5	5.1	426	2	Q5XMR6_9HEPC	Q5xmr6 hepatitis c	369	87	5.0	1924	2	Q4SDG6_TETNG	Q4sdg6 tetraodon n
297	88.5	5.1	426	2	Q5XMR7_9HEPC	Q5xmr7 hepatitis c	370	86.5	5.0	334	1	FCN1_MOUSE	Q70165 mus musculus
298	88.5	5.1	426	2	Q5XMR8_9HEPC	Q5xmr8 hepatitis c	371	86.5	5.0	334	2	Q4FJMI_MOUSE	Q4fjmi mus musculus
299	88.5	5.1	426	2	Q5XMR9_9HEPC	Q5xmr9 hepatitis c	372	86.5	5.0	364	2	Q7RC04_PLAYO	Q7rc04 plasmodium
300	88.5	5.1	426	2	Q5XN43_9HEPC	Q5xn43 hepatitis c	373	86.5	5.0	371	2	Q7M569_BRARE	Q7m569 brachydanio
301	88.5	5.1	426	2	Q5XN66_9HEPC	Q5xn66 hepatitis c	374	86.5	5.0	371	2	Q7T2P7_BRARE	Q7t2p7 brachydanio
302	88.5	5.1	497	2	Q5G5I7_9HETE	Q5g5i7 mrakia psyc	375	86.5	5.0	426	2	Q5XMR1_9HEPC	Q5xmr1 hepatitis c
303	88.5	5.1	507	2	Q00079_ASPPG	Q00079 aspergillus	376	86.5	5.0	426	2	Q5XN29_9HEPC	Q5xn29 hepatitis c
304	88.5	5.1	741	1	FIBA_CHICK	P14448 gallus gall	377	86.5	5.0	426	2	Q5XN49_9HEPC	Q5xn49 hepatitis c
305	88.5	5.1	764	2	Q6GNK6_XENLA	Q6gnk6 xenopus lae	378	86.5	5.0	426	2	Q5XN50_9HEPC	Q5xn50 hepatitis c
306	88.5	5.1	851	2	Q93MT4_PHOLU	Q93mt4 photorhabdu	379	86.5	5.0	426	2	Q5XN68_9HEPC	Q5xn68 hepatitis c
307	88.5	5.1	939	2	Q5SF31_HAEIN	Q5sf31 haemophilus	380	86.5	5.0	426	2	Q5XN95_9HEPC	Q5xn95 hepatitis c
308	88.5	5.1	1644	2	Q4PQU0_9HEPC	Q4pqu0 hepatitis c	381	86.5	5.0	426	2	Q5XND7_9HEPC	Q5xnd7 hepatitis c
309	88.5	5.1	2908	2	Q6LX04_9HEPC	Q6lx04 hepatitis c	382	86.5	5.0	470	2	Q9RH53_ENTAG	Q9rh53 enterobacte
310	88	5.0	243	2	Q18804_CABEL	Q18804 caenorhabdi	383	86.5	5.0	576	2	Q4KP49_9HEPC	Q4kp49 hepatitis c
311	88	5.0	326	1	FCN1_HUMAN	O00502 homo sapien	384	86.5	5.0	604	2	Q63KV4_BURPS	Q63kv4 burkholderi
312	88	5.0	326	2	Q5VVV5_HUMAN	Q5vvv5 homo sapien	385	86.5	5.0	604	2	Q4V2J8_BURMA	Q4v2j8 burkholderi
313	88	5.0	337	1	NCA3_YEAST	P46955 saccharomyc	386	86.5	5.0	613	2	Q6FUY9_CANGA	Q6fuy9 candida gla
314	88	5.0	337	2	Q6Q5N8_YEAST	Q6q5n8 saccharomyc	387	86.5	5.0	641	1	SSY1_SOLTU	P93568 solanum tub
315	88	5.0	485	2	Q8RLU2_PAEPO	Q8rlu2 paenibacill	388	86.5	5.0	726	2	Q9LAE4_AZOIR	Q9lae4 azospirillu
316	88	5.0	507	2	Q6QDD7_P9HAB	Q6qdd7 viral hemor	389	86.5	5.0	760	2	Q7ZTR1_XENLA	Q7ztr1 xenopus lae
317	88	5.0	564	2	Q9P8G8_PICAN	Q9p8g8 pichia anqu	390	86.5	5.0	2067	2	Q59ED8_HUMAN	Q59ed8 homo sapien
318	88	5.0	585	2	Q7N181_GLOVI	Q7n181 gloeobacter	391	86.5	5.0	2555	1	Q5XNM3_HUMAN	Q5xnm3 homo sapien
319	88	5.0	687	2	Q74PC8_YERPE	Q74pc8 yersinia pe	392	86.5	5.0	2556	1	NOTC1_HUMAN	P46531 homo sapien
320	88	5.0	687	2	Q8Z9W0_YERPE	Q8z9w0 yersinia pe	393	86	4.9	324	2	Q5ASW8_EMENI	Q5asw8 aspergillus
321	88	5.0	787	2	Q63X79_BURPS	Q63x79 burkholderi	394	86	4.9	346	2	Q6FL83_CANGA	Q6fl83 candida gla
322	88	5.0	787	2	Q62MM5_BURMA	Q62mm5 burkholderi	395	86	4.9	376	1	OMPC_SERMA	Q54471 serratia ma
323	88	5.0	896	2	Q52B52_MAGGR	Q52b52 magnaporthe	396	86	4.9	407	2	Q9DER1_CHICK	Q9der1 gallus gall

397	86	4.9	441	2	Q9DER0_CHICK	Q9der0 gallus gall	470	85	4.9	649	2	Q4IPS8_GIBZE	Q4ips8 gibberella
398	86	4.9	450	2	Q67119_9INFA	Q67119 influenza a	471	85	4.9	670	2	Q419J1_GIBZE	Q419j1 gibberella
399	86	4.9	453	2	Q9DER2_CHICK	Q9der2 gallus gall	472	85	4.9	677	2	Q663W5_YERPS	Q663w5 yersinia ps
400	86	4.9	564	1	HEMA_IASE2	P19701 influenza a	473	85	4.9	687	2	Q8WYE4_THEME	Q8wye4 thermotoga
401	86	4.9	575	2	Q49GX5_BRAJA	Q89gx5 bradyrhizob	474	85	4.9	764	2	Q8MYE4_THEME	Q8mye4 thermotoga
402	86	4.9	662	2	Q49RF7_PLABE	Q4yrf7 plasmodium	475	85	4.9	840	2	Q8FAY6_ECOL6	Q8fay6 escherichia
403	86	4.9	792	2	Q7NNR7_GLOVI	Q7nnr7 gloeobacter	476	85	4.9	843	2	Q8FAQ3_ECOL6	Q8faq3 escherichia
404	86	4.9	1028	2	Q8AS80_BACTN	Q8as80 bacteroides	477	85	4.9	971	2	Q68XX4_RICTY	Q68xx4 rickettsia
405	86	4.9	1230	2	Q4N8Y9_THEPA	Q4n8y9 theileria p	478	85	4.9	999	2	Q8A365_BACTN	Q8a365 bacteroides
406	86	4.9	1356	1	TENR_RAT	Q05546 rattus norv	479	85	4.9	1011	2	Q4WG05_ASPFU	Q4wg05 aspergillus
407	86	4.9	1391	2	Q48YC9_TETNG	Q48yc9 tetraodon n	480	85	4.9	1358	1	TENR_MOUSE	Q8by19 mus musculus
408	86	4.9	1453	2	Q755D1_ASHGO	Q755d1 ashbya gos	481	85	4.9	2472	2	Q14214_HUMAN	Q14214 homo sapien
409	86	4.9	1968	2	Q5QC18_LACRE	Q5qc18 lactobacill	482	85	4.9	2796	1	CSND3_MOUSE	Q80t79 mus musculus
410	86	4.9	2179	1	K0310_HUMAN	Q15027 homo sapien	483	85	4.9	2809	1	FEN3_HUMAN	Q75n90 homo sapien
411	85.5	4.9	228	2	O8EL80_OCEIH	Q8el80 oceanobacil	484	85	4.9	3867	2	Q53QQ2_HUMAN	Q53qq2 homo sapien
412	85.5	4.9	358	1	GLNA_CRYNE	Q96u99 cryptococcu	485	84.5	4.9	3669	1	NEBU_HUMAN	P20q29 homo sapien
413	85.5	4.9	358	1	OMPF_SERMA	Q55280 cryptococcu	486	84.5	4.8	197	2	Q72U30_LEPIC	Q72u30 leptospira
414	85.5	4.9	374	1	Q4WJ22_ASPFU	Q4wj22 aspergillus	487	84.5	4.8	231	2	Q5SPR3_BRARE	Q5spp3 brachydanio
415	85.5	4.9	426	2	Q5XN26_9HEPC	Q5xn26 hepatitis c	488	84.5	4.8	237	2	O31176_NEIME	O31176 neisseria m
416	85.5	4.9	426	2	Q5XN42_9HEPC	Q5xn42 hepatitis c	489	84.5	4.8	278	2	Q7XN46_ORISA	Q7xh46 oryza sativ
417	85.5	4.9	426	2	Q5XN52_9HEPC	Q5xn52 hepatitis c	490	84.5	4.8	278	2	Q8S5D6_ORISA	Q8s5d6 oryza sativ
418	85.5	4.9	426	2	Q5XN73_9HEPC	Q5xn73 hepatitis c	491	84.5	4.8	318	2	Q7XKC3_ORISA	Q7xkc3 oryza sativ
419	85.5	4.9	426	2	Q5XN76_9HEPC	Q5xn76 hepatitis c	492	84.5	4.8	380	2	Q5BA96_EMENI	Q5ba96 aspergillus
420	85.5	4.9	426	2	Q5XN91_9HEPC	Q5xn91 hepatitis c	493	84.5	4.8	381	2	Q8EY32_LEPIN	Q8ey32 leptospira
421	85.5	4.9	426	2	Q5XNE0_9HEPC	Q5xne0 hepatitis c	494	84.5	4.8	390	2	Q90G89_CHICK	Q90g89 caenorhabdi
422	85.5	4.9	426	2	Q5XNE4_9HEPC	Q5xne4 hepatitis c	495	84.5	4.8	399	2	Q5LGH1_BACFN	Q5lgh1 bacteroides
423	85.5	4.9	426	2	Q5XNE5_9HEPC	Q5xne5 hepatitis c	496	84.5	4.8	426	2	Q5XN51_9HEPC	Q5xn51 hepatitis c
424	85.5	4.9	426	2	Q5XN77_9HEPC	Q5xn77 hepatitis c	497	84.5	4.8	426	2	Q5XN58_9HEPC	Q5xn58 hepatitis c
425	85.5	4.9	436	1	FIEG_MOUSE	Q9vcn7 mus musculu	498	84.5	4.8	426	2	Q5XN67_9HEPC	Q5xn67 hepatitis c
426	85.5	4.9	468	1	ANVB_BACFI	P96513 bacillus fi	499	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
427	85.5	4.9	476	2	Q4WJ22_ASPFU	Q4wj22 aspergillus	500	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
428	85.5	4.9	484	2	Q4WJ22_ASPFU	Q4wj22 aspergillus	501	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
429	85.5	4.9	566	2	Q84110_9INFA	Q84110 influenza a	502	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
430	85.5	4.9	566	2	Q84110_9INFA	Q84110 influenza a	503	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
431	85.5	4.9	568	2	Q70J58_ASPFU	Q70j58 aspergillus	504	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
432	85.5	4.9	594	2	Q4WJ22_ASPFU	Q4wj22 aspergillus	505	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
433	85.5	4.9	670	2	Q9EWU9_STRCO	Q9ewu9 streptomyce	506	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
434	85.5	4.9	722	2	P96091_TREDE	P96091 treponema d	507	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
435	85.5	4.9	804	2	O00089_ASPNG	O00089 aspergillus	508	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
436	85.5	4.9	804	2	O00089_ASPNG	O00089 aspergillus	509	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
437	85.5	4.9	866	1	FIBA_HUMAN	P02671 homo sapien	510	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
438	85.5	4.9	915	2	Q4QL82_HAEI8	Q4ql82 haemophilus	511	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
439	85.5	4.9	915	2	Q5SFH9_HAEIN	Q5sfh9 haemophilus	512	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
440	85.5	4.9	950	2	Q5DNB1_CLOPE	Q5dnb1 clostridium	513	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
441	85.5	4.9	1358	1	TENR_HUMAN	P12107 homo sapien	514	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
442	85.5	4.9	1806	1	CORAI_HUMAN	Q88207 mus musculu	515	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
443	85.5	4.9	1838	2	O88207_MOUSE	Q60467 cricetus	516	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
444	85.5	4.9	1840	2	Q60467_CRILLO	Q9ji03 rattus norv	517	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
445	85.5	4.9	2475	2	Q501R6_XENTR	Q501r6 xenopus tro	518	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
446	85.5	4.9	2475	2	Q501R6_XENTR	Q501r6 xenopus tro	519	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
447	85.5	4.9	2850	1	HORN_HUMAN	Q86y23 homo sapien	520	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
448	85.5	4.9	2850	1	HORN_HUMAN	Q86y23 homo sapien	521	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
449	85.5	4.9	2850	2	Q5ULF4_HUMAN	Q5ulf4 homo sapien	522	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
450	85	4.9	295	2	Q5DT20_HUMAN	Q5dt20 homo sapien	523	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
451	85	4.9	303	2	Q8H3E2_ORISA	Q8h3e2 oryza sativ	524	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
452	85	4.9	314	2	Q51041_XENLA	Q51041 xenopus lae	525	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
453	85	4.9	314	2	Q5PRF5_XENLA	Q5prf5 xenopus lae	526	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
454	85	4.9	320	2	Q5AUM3_EMENI	Q5aum3 aspergillus	527	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
455	85	4.9	321	2	Q5HFS9_ASPAC	Q5hfs9 aspergillus	528	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
456	85	4.9	330	2	Q5TPG6_ANOGA	Q5tpg6 anopheles g	529	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
457	85	4.9	331	2	Q87Q71_VIBPA	Q87q71 vibrio para	530	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
458	85	4.9	338	2	Q6DIT6_XENTR	Q6dit6 xenopus tro	531	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
459	85	4.9	343	2	Q6DJE9_XENLA	Q6dje9 xenopus lae	532	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
460	85	4.9	356	2	Q9HR20_HALSA	Q9hr20 halobacteri	533	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
461	85	4.9	356	2	Q95P98_HALRO	Q95p98 halocynthia	534	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
462	85	4.9	414	2	Q61KT2_CABBR	Q61kt2 caenorhabdi	535	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
463	85	4.9	420	2	Q4IF74_GIBZE	Q4if74 gibberella	536	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
464	85	4.9	426	2	Q5XNK1_9HEPC	Q5xnk1 hepatitis c	537	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
465	85	4.9	430	2	Q4WDJ5_ASPFU	Q4wdj5 aspergillus	538	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
466	85	4.9	464	2	Q82LA2_STRAW	Q82la2 streptomyce	539	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
467	85	4.9	550	2	Q64MM2_BACFR	Q64mm2 bacteroides	540	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
468	85	4.9	552	2	Q6DWT7_9INFA	Q6dwt7 influenza a	541	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
469	85	4.9	554	2	Q5L7G1_BACFN	Q5l7g1 bacteroides	542	84	4.8	426	2	Q5XN69_9HEPC	Q5xn69 bacteroides
			556	2	Q6DXG9_9INFA	Q6dxg9 influenza a							

543	84	4.8	555	2	Q6BGR4_ORYSA	Q6b6z4_oryza sativ	616	83	4.8	240	2	Q61H40_CABBR	Q61h40_caenorhabdi
544	84	4.8	565	1	Q82544_9INFA	Q82544_influenza a	617	83	4.8	254	2	Q5XK70_XENLA	Q5xk70_xenopus lae
545	84	4.8	586	1	INV3_ORYSA	Q56ud3_oryza sativ	618	83	4.8	317	2	Q5QTR2_HUMAN	Q5qtr2_xenopus tro
546	84	4.8	597	2	Q96459_STRPU	Q96459_strongyloce	619	83	4.8	319	2	Q5FW10_XENTR	Q5fw10_xenopus tro
547	84	4.8	638	2	Q9VNX8_DROME	Q9vnx8_drosophila	620	83	4.8	363	2	Q45822_CABEL	Q45822_caenorhabdi
548	84	4.8	684	2	Q6DHS2_BRACE	Q6dhs2_brachydanio	621	83	4.8	367	2	Q70EWA_HONGA	Q70ewa_homarus gam
549	84	4.8	782	1	FIBA_RAT	P06399_rattus norv	622	83	4.8	371	2	Q5MIY7_ABDAL	Q5miy7_aedes albop
550	84	4.8	782	1	Q7TQ70_RAT	Q7tq70_rattus norv	623	83	4.8	401	2	Q5YUT6_BIOGL	Q5yut6_biophalari
551	84	4.8	836	1	PAPC_ECOLI	P07110_escherichia	624	83	4.8	407	2	Q9PU54_CHICK	Q9pu54_gallus gall
552	84	4.8	836	1	Q8GA01_ECOLI	Q8ga01_escherichia	625	83	4.8	413	2	Q84582_STRAU	Q84582_streptomyce
553	84	4.8	839	2	Q4FPG3_ECOLI	Q4fbg3_escherichia	626	83	4.8	426	2	Q5XNJ6_9HEPC	Q5xnj6_hepatitis c
554	83.5	4.8	257	1	MFAE4_MOUSE	Q9dlh9_mus musculus	627	83	4.8	432	2	Q7UUR7_RHOBA	Q7uur7_rhodopirella
555	83.5	4.8	266	1	Q7QGR8_ANOGA	Q7qgr8_anopheles g	628	83	4.8	459	2	Q7Z7X3_TRIVI	Q7z7x3_trichodermma
556	83.5	4.8	268	2	Q6VFN2_ANOGA	Q6vpn2_anopheles g	629	83	4.8	493	2	Q6QHT4_BACCI	Q6qht4_bacillus ci
557	83.5	4.8	268	2	Q6VFN3_ANOGA	Q6vpn3_anopheles g	630	83	4.8	501	1	HDAC_ARATH	Q22446_arabidopsis
558	83.5	4.8	279	2	Q7ZT73_XENLA	Q7zt73_xenopus lae	631	83	4.8	507	2	Q6QDD6_9RHAB	Q6qdd6_viral hemor
559	83.5	4.8	308	2	Q17452_CABEL	Q17452_caenorhabdi	632	83	4.8	513	2	Q9LHQ8_ARATH	Q9lqh8_arabidopsis
560	83.5	4.8	337	1	ANGU7_MOUSE	Q8riaq3_mus musculus	633	83	4.8	526	2	Q742T0_MYCPA	Q742t0_mycobacteri
561	83.5	4.8	354	2	Q9UG11_DROAN	Q9ug11_drosophila	634	83	4.8	543	2	Q7QHL5_ANOGA	Q7qhl5_anopheles g
562	83.5	4.8	359	2	Q81188_DROVI	Q81188_drosophila	635	83	4.8	553	1	VH65_NEVAC	Q08539_autographa
563	83.5	4.8	392	2	Q39171_9INFA	Q39171_influenza a	636	83	4.8	564	2	Q84W45_ARATH	Q84w45_arabidopsis
564	83.5	4.8	426	2	Q5XML9_9HEPC	Q5xml9_hepatitis c	637	83	4.8	568	2	Q7Z4E9_HUMAN	Q7z4e9_homo sapien
565	83.5	4.8	426	2	Q5XMU0_9HEPC	Q5xmu0_hepatitis c	638	83	4.8	585	2	Q96EW9_HUMAN	Q96ew9_homo sapien
566	83.5	4.8	426	2	Q5XMU1_9HEPC	Q5xmu1_hepatitis c	639	83	4.8	585	2	Q96K81_HUMAN	Q96k81_homo sapien
567	83.5	4.8	426	2	Q5XMU3_9HEPC	Q5xmu3_hepatitis c	640	83	4.8	609	2	Q9BY44_HUMAN	Q9by44_homo sapien
568	83.5	4.8	426	2	Q5XN21_9HEPC	Q5xn21_hepatitis c	641	83	4.8	730	2	Q8DS80_STRMU	Q8ds80_streptococc
569	83.5	4.8	426	2	Q5XN65_9HEPC	Q5xn65_hepatitis c	642	83	4.8	737	2	Q8T316_PABLI	Q8t316_paracentrot
570	83.5	4.8	426	2	Q5XN70_9HEPC	Q5xn70_hepatitis c	643	83	4.8	760	2	Q8EA47_SHEON	Q8ea47_shewanella
571	83.5	4.8	426	2	Q5XN75_9HEPC	Q5xn75_hepatitis c	644	83	4.8	792	2	Q8ZRS1_SALTY	Q8zrs1_salmonella
572	83.5	4.8	426	2	Q5XN98_9HEPC	Q5xn98_hepatitis c	645	83	4.8	806	2	Q57T86_SALCH	Q57t86_salmonella
573	83.5	4.8	426	2	Q5XND8_9HEPC	Q5xnd8_hepatitis c	646	83	4.8	904	2	Q82NR8_STRAW	Q82nr8_streptomyce
574	83.5	4.8	426	2	Q5XNE1_9HEPC	Q5xne1_hepatitis c	647	83	4.8	914	2	Q9IF30_ADEBA	Q9if30_bovine aden
575	83.5	4.8	430	2	Q98N05_RHILLO	Q98n05_rhizobium l	648	83	4.8	977	2	Q4UNB6_RICFE	Q4unb6_rickettsia
576	83.5	4.8	441	2	O13337_MAGGR	O13337_magnaporthe	649	83	4.8	993	2	Q5LHN8_BACFN	Q5lhn8_bacteroides
577	83.5	4.8	451	2	Q8H788_ARATH	Q8h788_arabidopsis	650	83	4.8	1103	2	Q6MZP4_HUMAN	Q6mzp4_homo sapien
578	83.5	4.8	467	2	Q86WX2_HUMAN	Q86wx2_homo sapien	651	83	4.8	1309	2	Q64428_CHLVU	Q64428_chlorella v
579	83.5	4.8	467	2	Q8RWX7_ARATH	Q8rwx7_arabidopsis	652	83	4.8	1644	2	Q4PQ77_9HEPC	Q4pq77_hepatitis c
580	83.5	4.8	476	2	Q5T5Y9_HUMAN	Q5t5y9_homo sapien	653	83	4.8	2019	2	Q80YX2_MOUSE	Q80yx2_mus musculu
581	83.5	4.8	489	2	Q90218_BRARE	Q90218_brachydanio	654	83	4.8	2019	2	Q64706_MOUSE	Q64706_mus musculu
582	83.5	4.8	500	1	NIPD_BRASP	P06120_bradyrhizob	655	83	4.8	2110	2	Q80YX1_MOUSE	Q80yx1_mus musculu
583	83.5	4.8	543	2	Q7PC52_9ALTE	Q7pc52_saccharoph	656	83	4.8	2193	2	Q6MZM7_HUMAN	Q6mzm7_homo sapien
584	83.5	4.8	566	2	Q82545_9INFA	Q82545_influenza a	657	83	4.8	2217	2	Q585T2_HUMAN	Q585t2_homo sapien
585	83.5	4.8	566	2	Q82751_9ORTO	Q82751_unidentifie	658	83	4.8	2240	2	Q68DP8_HUMAN	Q68dp8_homo sapien
586	83.5	4.8	566	2	Q918Q7_9INFA	Q918q7_influenza a	659	83	4.8	2365	2	Q60FE4_HUMAN	Q60fe4_homo sapien
587	83.5	4.8	576	2	Q4KP40_9HEPC	Q4kp40_hepatitis c	660	83	4.8	2267	2	Q68DP9_HUMAN	Q68dp9_homo sapien
588	83.5	4.8	601	2	Q5ZMM1_CHICK	Q5zmm1_gallus gall	661	83	4.8	2296	2	Q6N0A6_HUMAN	Q6n0a6_homo sapien
589	83.5	4.8	608	2	Q82P56_STRAW	Q82p56_streptomyce	662	83	4.8	2351	2	Q59EHI_HUMAN	Q59ehi_homo sapien
590	83.5	4.8	613	2	Q4T5H8_TETNG	Q4t5h8_tetradodon n	663	83	4.8	2357	2	Q68DT4_HUMAN	Q68dt4_homo sapien
591	83.5	4.8	688	2	Q9SHY2_ARATH	Q9shy2_arabidopsis	664	83	4.8	2386	1	FINC_HUMAN	P02751_homo sapien
592	83.5	4.8	698	2	Q83LL6_SHIFL	Q83ll6_shigella fl	665	83	4.8	2444	2	Q6N025_HUMAN	Q6n025_homo sapien
593	83.5	4.8	702	2	Q32747_9POAL	Q32747_oryzopsis r	666	83	4.8	2477	2	Q6MZU5_HUMAN	Q6mzu5_homo sapien
594	83.5	4.8	725	2	O52158_NEIME	Q52158_neisseria m	667	83	4.8	3010	2	Q5R2D7_9HEPC	Q5r2d7_hepatitis c
595	83.5	4.8	764	2	Q6PH33_XANAC	Q6ph33_xanthomonas	668	82.5	4.7	226	2	Q4RDUI_TETNG	Q4rdui_tetradodon n
596	83.5	4.8	796	2	Q5PD44_SALPA	Q5pd44_salmonella	669	82.5	4.7	246	2	Q81X22_9TREM	Q81x22_opisthorchi
597	83.5	4.8	870	2	Q4UTW2_XANCP	Q4utw2_xanthomonas	670	82.5	4.7	307	2	Q5ZR75_CABEL	Q5zr75_caenorhabdi
598	83.5	4.8	870	2	Q8P9S3_XANCP	Q8p9s3_xanthomonas	671	82.5	4.7	312	1	FGL1_HUMAN	Q52z75_caenorhabdi
599	83.5	4.8	1017	2	Q59HB5_HUMAN	Q59hb5_homo sapien	672	82.5	4.7	312	2	Q8NG32_HUMAN	Q8ng32_homo sapien
600	83.5	4.8	1053	2	Q4RHV2_TETNG	Q4rhv2_tetradodon n	673	82.5	4.7	312	2	Q53YF1_HUMAN	Q53yf1_homo sapien
601	83.5	4.8	1109	2	Q64VL9_BACFR	Q64vl9_bacteroides	674	82.5	4.7	312	2	Q4FJH9_HUMAN	Q4fjh9_homo sapien
602	83.5	4.8	1233	2	Q6ZSN4_HUMAN	Q6zsn4_homo sapien	675	82.5	4.7	388	1	ANGL5_HUMAN	Q59702_schizosacch
603	83.5	4.8	1379	2	Q6T256_HUMAN	Q6t256_homo sapien	676	82.5	4.7	405	1	CLR6_SCHPO	Q5xnm3_hepatitis c
604	83.5	4.8	1588	2	Q8XKX8_CLOPE	Q8xxk8_clostridium	677	82.5	4.7	426	2	Q5XNM3_9HEPC	Q5xnm3_hepatitis c
605	83.5	4.8	1644	2	Q4PQT4_9HEPC	Q4pqt4_hepatitis c	678	82.5	4.7	426	2	Q5XN53_9HEPC	Q5xn53_hepatitis c
606	83.5	4.8	1644	2	Q4PQT3_9HEPC	Q4pqt3_hepatitis c	679	82.5	4.7	455	2	Q5XN74_9HEPC	Q5xn74_hepatitis c
607	83.5	4.8	1644	2	Q4PQT2_9HEPC	Q4pqt2_hepatitis c	680	82.5	4.7	460	2	Q82AS5_STRAW	Q82as5_streptomyce
608	83.5	4.8	1806	2	Q5VT31_HUMAN	Q5vt31_homo sapien	681	82.5	4.7	489	2	Q8RQC5_TETNG	Q8rqc5_tetradodon n
609	83.5	4.8	2391	2	Q7XR12_ORYSA	Q7xr12_oryza sativ	682	82.5	4.7	489	2	Q6GP67_XENLA	Q6gp67_xenopus lae
610	83.5	4.8	3411	2	Q6PX46_9FLAV	Q6px46_yellow feve	683	82.5	4.7	502	2	Q8GWU4_ARATH	Q8gwu4_arabidopsis
611	83.5	4.8	3411	2	Q6J3P1_9FLAV	Q6j3p1_yellow feve	684	82.5	4.7	502	2	Q8ZNS2_SALTY	Q8zns2_salmonella
612	83.5	4.8	3471	2	Q6HBX5_BACHK	Q6hbx5_bacillus th	685	82.5	4.7	564	2	Q4KPF4_9HEPC	Q4kpf4_hepatitis c
613	83.5	4.8	4163	2	Q9LAE6_RHILT	Q9lae6_rhizobium l	686	82.5	4.7	576	2	Q8VR37_ECOLI	Q8vr37_escherichia
614	83.5	4.8	5839	2	Q5RGP8_BRARE	Q5rgp8_brachydanio	687	82.5	4.7	587	2	Q86HC0_HUMAN	Q86hc0_homo sapien
615	83	4.8	169	2	Q868G5_9ACAR	Q868g5_amblyomma a	688	82.5	4.7	591	2		



835	81	4.6	404	2	Q4RXV0_TETNG	Q4RXV0 tetraodon n	908	80.5	4.6	455	1	ANGL3_MOUSE	Q9r182 mus musculus
836	81	4.6	432	1	FGL2_MOUSE	P12804 mus musculus	909	80.5	4.6	473	2	O70605_RAT	O70605 rattus norv
837	81	4.6	432	1	Q544K3_MOUSE	Q544k3 mus musculus	910	80.5	4.6	548	1	THER_BACST	P06874 bacillus st
838	81	4.6	445	2	O5G3N2_ENTFA	Q5g3n2 enterococcu	911	80.5	4.6	576	2	Q4KP36_9HEPC	Q4kp36 hepatitis c
839	81	4.6	447	2	O82YLO_ENTFA	Q82ylo enterococcu	912	80.5	4.6	576	2	Q4KP37_9HEPC	Q4kp37 hepatitis c
840	81	4.6	507	2	Q6QDE6_9RHAB	Q6qde6 viral memor	913	80.5	4.6	576	2	Q4KP38_9HEPC	Q4kp38 hepatitis c
841	81	4.6	513	2	Q90Z19_BRARE	Q90z19 brachydanio	914	80.5	4.6	576	2	Q4KP39_9HEPC	Q4kp39 hepatitis c
842	81	4.6	518	2	Q5LH40_BACFN	Q5lh40 bacteroides	915	80.5	4.6	576	2	Q4KP45_9HEPC	Q4kp45 hepatitis c
843	81	4.6	518	2	Q64XZ7_BACFR	Q64xz7 bacteroides	916	80.5	4.6	629	2	Q4HU61_GIBZE	Q4hu61 gibberella
844	81	4.6	528	2	Q13344_HUMAN	Q13344 homo sapien	917	80.5	4.6	728	2	Q7QBP4_ANOGA	Q7qbp4 anopheles g
845	81	4.6	548	1	AMT4_PSEST	P13507 pseudomonas	918	80.5	4.6	733	2	Q8EDM8_SHEON	Q8edm8 shewanella
846	81	4.6	576	2	Q7VVU6_BORPE	Q7vvu6 bordetella	919	80.5	4.6	748	2	Q4HXL9_GIBZE	Q4hxl9 gibberella
847	81	4.6	603	2	Q9M040_ARATH	Q9m040 arabidopsis	920	80.5	4.6	778	2	Q04184_9HEPC	Q04184 hepatitis c
848	81	4.6	605	2	Q8T525_TRISP	Q8t525 trichinella	921	80.5	4.6	803	2	Q934J0_9BACL	Q934j0 paenibacill
849	81	4.6	668	2	Q8K0W0_MOUSE	Q8k0w0 mus musculus	922	80.5	4.6	815	2	Q80B16_9HEPC	Q80b16 hepatitis c
850	81	4.6	691	2	Q6AZ11_XENLA	Q6az11 xenopus lae	923	80.5	4.6	841	2	Q92J88_HELPJ	Q92j88 helicobacte
851	81	4.6	726	2	O6V7U2_9VIRU	Q6v7u2 snake parvo	924	80.5	4.6	867	1	SFMD_ECOLI	P77468 escherichia
852	81	4.6	767	2	Q9QUD8_9VIRU	Q9qud8 torque teno	925	80.5	4.6	869	2	Q7AGT8_ECO57	Q7agt8 escherichia
853	81	4.6	792	1	OSTA_XYLFA	Q9pf41 xyella fas	926	80.5	4.6	869	2	Q8XCT4_ECO57	Q8xct4 escherichia
854	81	4.6	792	1	OSTA_XYLFA	Q87ai9 xyella fas	927	80.5	4.6	889	2	Q6XLI6_FUGRU	Q6xli6 fugu rubrip
855	81	4.6	817	2	Q9RY85_DEIRA	P73619 synechocyst	928	80.5	4.6	921	2	Q6CFT8_YARLI	Q6cfi8 yarrowia li
856	81	4.6	872	2	Q9RY85_DEIRA	Q9ry85 deinococcus	929	80.5	4.6	955	2	Q21750_CABEL	Q21750 caenorhabdi
857	81	4.6	873	2	Q5YZV6_NOCFA	Q5yzv6 nocardia fa	930	80.5	4.6	994	1	EPHB2_MOUSE	P54763 mus musculus
858	81	4.6	890	2	O86727_STRCO	O86727 streptomyce	931	80.5	4.6	998	2	Q9HLO9_THBAC	Q9hlo9 thermoplasm
859	81	4.6	902	1	FTHFD_HUMAN	O75891 homo sapien	932	80.5	4.6	1001	2	Q58M71_9CAUD	Q58m71 cyanophage
860	81	4.6	902	2	Q53H87_HUMAN	Q53h87 homo sapien	933	80.5	4.6	1021	2	O6GT07_MOUSE	O6gt07 mus musculus
861	81	4.6	940	2	O8Y4N9_LISMO	O8y4n9 listeria mo	934	80.5	4.6	1029	2	O6P5F1_MOUSE	O6p5f1 mus musculus
862	81	4.6	954	2	O59G10_HUMAN	O59g10 homo sapien	935	80.5	4.6	1100	2	Q8A2Y1_BACTN	Q8a2y1 bacteroides
863	81	4.6	1028	2	O68083_RHOCA	O68083 rhodobacter	936	80.5	4.6	1254	2	Q8V291_9VIRU	Q8v291 venezuelan
864	81	4.6	1082	2	Q6N3Z4_RHOPA	Q6n3z4 rhodopseudo	937	80.5	4.6	1254	2	Q8V293_9VIRU	Q8v293 venezuelan
865	81	4.6	1349	2	Q6CW00_KULJA	Q6cw00 kluyveriomye	938	80.5	4.6	1254	2	Q9YK03_9VIRU	Q9yk03 venezuelan
866	81	4.6	1628	2	Q6C1S4_YARLI	Q6c1s4 yarrowia li	939	80.5	4.6	1254	2	Q5IBC2_9VIRU	Q5ibc2 venezuelan
867	81	4.6	1785	2	O9Y4V9_HUMAN	O9y4v9 homo sapien	940	80.5	4.6	1264	2	Q8UYH1_9VIRU	Q8uyh1 venezuelan
868	81	4.6	1785	2	Q5JR23_HUMAN	Q5jr23 homo sapien	941	80.5	4.6	1480	2	Q5B715_EMENI	Q5b715 aspergillus
869	81	4.6	1785	2	Q9T211_HUMAN	Q9t211 homo sapien	942	80.5	4.6	1644	2	Q4PQ07_9HEPC	Q4pq07 hepatitis c
870	81	4.6	1819	2	Q4TT23_9SPHN	Q4tt23 erythrobaact	943	80.5	4.6	1644	2	Q4PQ08_9HEPC	Q4pq08 hepatitis c
871	81	4.6	2403	2	Q9UGM2_HUMAN	Q9ugm2 homo sapien	944	80.5	4.6	1644	2	Q4PQ08_9HEPC	Q4pq08 hepatitis c
872	81	4.6	2403	2	Q5JR22_HUMAN	Q5jr22 homo sapien	945	80.5	4.6	1644	2	Q4PQ07_9HEPC	Q4pq07 hepatitis c
873	81	4.6	2413	2	Q9UKJ4_HUMAN	Q9ukj4 homo sapien	946	80.5	4.6	1804	1	COBA1_MOUSE	O61245 mus musculus
874	81	4.6	2413	2	Q96DU4_HUMAN	Q96du4 homo sapien	947	80.5	4.6	1804	2	Q80WR4_MOUSE	Q80wr4 mus musculus
875	81	4.6	2413	2	Q5JR26_HUMAN	Q5jr26 homo sapien	948	80.5	4.6	1912	2	Q29528_PAPHA	Q29528 papio hamad
876	81	4.6	2426	2	Q9UGM3_HUMAN	Q9ugm3 homo sapien	949	80.5	4.6	1928	2	Q4PE06_USTMA	Q4pe06 ustilago ma
877	81	4.6	2542	2	Q5JR25_HUMAN	Q5jr25 homo sapien	950	80.5	4.6	2039	1	CR1_HUMAN	P17927 homo sapien
878	81	4.6	3670	1	C5ND3_HUMAN	Q5oft9 campylobact	951	80.5	4.6	2039	2	Q5SR43_HUMAN	Q5sr43 homo sapien
879	80.5	4.6	140	2	Q5OPT9_CAMJE	Q5oft9 campylobact	952	80.5	4.6	2039	2	Q5SR44_HUMAN	Q5sr44 homo sapien
880	80.5	4.6	164	2	Q855P8_9CAUD	Q855p8 mycobacteri	953	80.5	4.6	2039	2	Q5SR45_HUMAN	Q5sr45 homo sapien
881	80.5	4.6	180	2	Q7Q214_ANOGA	Q7q214 anopheles g	954	80.5	4.6	2322	2	Q5UDW6_PLAFA	Q5udw6 plasmodium
882	80.5	4.6	211	2	Q7QHK4_ANOGA	Q7qhk4 anopheles g	955	80.5	4.6	166	2	P74440_SYNY3	P74440 synechocyst
883	80.5	4.6	220	2	Q7R7G6_PLAYO	Q7r7g6 plasmodium	956	80	4.6	166	2	Q7PAW6_RICSI	Q7paw6 rickettsia
884	80.5	4.6	223	2	Q5DLF1_BRARE	Q5blf1 brachydanio	957	80	4.6	177	2	Q6EKX1_BIOGL	Q6ekx1 biophalari
885	80.5	4.6	293	2	Q5DHL9_SCHJA	Q5dhl9 schistosoma	958	80	4.6	177	2	Q6EKX5_BIOGL	Q6ekx5 biophalari
886	80.5	4.6	300	2	Q8VD40_CAVPO	Q8vd40 cavia porce	959	80	4.6	217	2	Q95UV7_BIOGL	Q95uv7 biophalari
887	80.5	4.6	315	2	Q98UL0_9HEPC	Q98ul0 hepatitis c	960	80	4.6	297	2	Q34879_BACSU	Q34879 bacillus su
888	80.5	4.6	319	2	O43015_SCHPO	O43015 schistosacch	961	80	4.6	308	2	Q5FW50_XENTR	Q5fw50 xenopus tro
889	80.5	4.6	334	2	O62135_CABEL	O62135 caenorhabdi	962	80	4.6	310	2	Q5U6G7_BETVU	Q5u6g7 beta vulgar
890	80.5	4.6	342	2	Q9TXW7_CABEL	Q9txw7 caenorhabdi	963	80	4.6	318	2	Q6ZNF8_HUMAN	Q6znf8 homo sapien
891	80.5	4.6	343	2	Q9JFW5_9INFA	Q9jfv5 influenza a	964	80	4.6	318	2	Q6ZQW8_HUMAN	Q6zqw8 homo sapien
892	80.5	4.6	371	2	Q63LNA_BURPS	Q63ln4 burkholderi	965	80	4.6	355	2	Q5CQX2_CRIPIV	Q5cqx2 cryptospori
893	80.5	4.6	371	2	Q62BQ4_BURMA	Q62bq4 burkholderi	966	80	4.6	395	1	DNAJ2_CORGL	Q8nly8 corynebacte
894	80.5	4.6	398	2	Q8A095_BACTN	Q8a095 bacteroides	967	80	4.6	397	2	Q5AXX1_EMENI	Q5axx1 aspergillus
895	80.5	4.6	406	2	Q9S4K6_ECOLI	Q9s4k6 escherichia	968	80	4.6	406	2	Q4UGB1_THEAN	Q4ugb1 theileria a
896	80.5	4.6	418	2	Q95L38_BOVIN	Q95l38 bos taurus	969	80	4.6	405	1	PDC2_PEA	P51851 pium sativ
897	80.5	4.6	421	2	Q4TC97_TETNG	Q4tc97 tetraodon n	970	80	4.6	411	2	Q54TD6_DICDI	Q54td6 dictyosteli
898	80.5	4.6	425	2	Q3UPP7_NEIME	Q3jpp7 neisseria m	971	80	4.6	414	2	Q5V6U3_HALMA	Q5v6u3 haloarcula
899	80.5	4.6	426	2	Q5XML8_9HEPC	Q5xml8 hepatitis c	972	80	4.6	426	2	Q6ZS27_HUMAN	Q6zsz7 homo sapien
900	80.5	4.6	426	2	Q5XMM0_9HEPC	Q5xmm0 hepatitis c	973	80	4.6	426	2	Q5XNJ5_9HEPC	Q5xnj5 hepatitis c
901	80.5	4.6	426	2	Q5XMM8_9HEPC	Q5xmm8 hepatitis c	974	80	4.6	426	2	Q5XNK3_9HEPC	Q5xnk3 hepatitis c
902	80.5	4.6	426	2	Q5XMM8_9HEPC	Q5xmm8 hepatitis c	975	80	4.6	439	1	FGL2_HUMAN	Q14314 homo sapien
903	80.5	4.6	426	2	Q5XMK3_9HEPC	Q5xmkn3 hepatitis c	976	80	4.6	439	2	Q53GD2_HUMAN	Q53gd2 homo sapien
904	80.5	4.6	426	2	Q5XNK4_9HEPC	Q5xnk4 hepatitis c	977	80	4.6	439	2	Q5F311_CHICK	Q5f311 gallus gall
905	80.5	4.6	426	2	Q5XN77_9HEPC	Q5xn77 hepatitis c	978	80	4.6	454	2	Q8GXT3_ARATH	Q8gxt3 arabidopsis
906	80.5	4.6	426	2	Q5XNC5_9HEPC	Q5xnc5 hepatitis c	979	80	4.6	489	2	Q74313_MYCPA	Q74313 mycobacteri
907	80.5	4.6	426	2	Q5XNC9_9HEPC	Q5xnc9 hepatitis c	980	80	4.6	497	2	Q4NL96_WMICC	Q4nl96 arthrobacte



981	80	4.6	519	2	Q55J76_CRYNE	Q55j16 cryptococcu	1054	79.5	4.6	426	2	Q5XWV3_9HEPC	Q5XWV3 hepatitis c
982	80	4.6	519	2	Q5KA05_CRYNE	Q5ka05 cryptococcu	1055	79.5	4.6	426	2	Q5XWV4_9HEPC	Q5XWV4 hepatitis c
983	80	4.6	534	2	Q9RBJ1_ACEDI	Q9rbj1 acetobacter	1056	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
984	80	4.6	538	2	Q74D86_GEOSL	Q74d86 geobacter s	1057	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
985	80	4.6	561	2	Q82764_9INFA	Q82764 influenza a	1058	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
986	80	4.6	565	2	Q82766_9INFA	Q82766 influenza a	1059	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
987	80	4.6	566	2	Q8UW70_9INFA	Q8uw70 influenza a	1060	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
988	80	4.6	574	2	Q8E9W9_SHEON	Q8e9w9 shewanella	1061	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
989	80	4.6	576	2	Q5B821_SWENI	Q5b821 aspergillus	1062	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
990	80	4.6	576	2	Q7M637_BORFA	Q7m637 bordetella	1063	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
991	80	4.6	576	2	Q7M103_BORBR	Q7m103 bordetella	1064	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
992	80	4.6	577	2	Q9L5C5_BURPS	Q9l5c5 burkholderi	1065	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
993	80	4.6	580	2	Q4QRJ7_BRARE	Q4qrj7 brachydanio	1066	79.5	4.6	426	2	Q5XWV7_9HEPC	Q5XWV7 hepatitis c
994	80	4.6	582	2	Q4V3B3_ARATH	Q4v3b3 arabidopsis	1067	79.5	4.6	441	1	TOLB_ANAMM	Q5XNB4 hepatitis c
995	80	4.6	584	2	Q4V706_DROME	Q4v706 drosophila	1068	79.5	4.6	474	2	Q8L0Y4_9MICO	Q8l0y4 terrabacter
996	80	4.6	593	2	Q8RUU6_MAIZE	Q8ruu6 zea mays (m	1069	79.5	4.6	482	2	Q6NVU1_HUMAN	Q6nvu1 homo sapien
997	80	4.6	597	2	Q9LGL5_ORYSA	Q9lgl5 oryza sativ	1070	79.5	4.6	500	2	Q759N6_ASHGO	Q759n6 ashbya goes
998	80	4.6	641	1	F1BAZ2_PETMA	P33573 petromyzon	1071	79.5	4.6	507	2	Q88983_9RHAB	Q88983 viral hemor
999	80	4.6	670	2	Q9FCR7_NEIMB	Q9fcr7 neisseria m	1072	79.5	4.6	517	2	Q93Z04_ARATH	Q93z04 arabidopsis
1000	80	4.6	671	2	Q8SXR9_DROME	Q8sxr9 drosophila	1073	79.5	4.6	536	2	Q4PC63_USTMA	Q4pc63 ustilago ma
1001	80	4.6	702	2	Q9TWV8_9POAL	Q9twv8 guaduella m	1074	79.5	4.6	566	2	Q9YTB9_9INFA	Q9ytb9 influenza a
1002	80	4.6	702	2	Q69749_NEIME	Q69749 neisseria m	1075	79.5	4.6	586	2	Q84XV1_MUSAC	Q84xv1 musa acumin
1003	80	4.6	737	2	Q7M9D6_WOLSU	Q7m9d6 wolfinella s	1076	79.5	4.6	606	2	Q8XP99_CLOPE	Q8xp99 clostridium
1004	80	4.6	762	2	Q41B99_GIBZE	Q41b99 gibberella s	1077	79.5	4.6	626	2	Q64599_ARATH	Q64599 arabidopsis
1005	80	4.6	785	2	Q50YB3_ENTHI	Q50yb3 entamoeba h	1078	79.5	4.6	672	2	Q613K3_CAEBR	Q613k3 caenorhabdi
1006	80	4.6	766	2	Q82K66_STRAW	Q82k66 streptomyce	1079	79.5	4.6	691	2	Q4SVM2_TETNG	Q4svm2 tetraodon n
1007	80	4.6	767	2	Q5WY55_BACSK	Q5wy55 bacillus cl	1080	79.5	4.6	706	1	TGM3L_HUMAN	Q95932 homo sapien
1008	80	4.6	771	2	Q8NJKX6_9FUNG	Q8njx6 piromyces s	1081	79.5	4.6	712	2	Q6FDG4_ACIAD	Q6fdg4 acinetobact
1009	80	4.6	778	2	Q8NJKX5_9FUNG	Q8njx5 piromyces s	1082	79.5	4.6	726	2	Q59HH9_VIBUD	Q59hh9 vibrio vuln
1010	80	4.6	811	2	Q5RBN3_PONPY	Q5rbn3 pongo pygma	1083	79.5	4.6	746	2	Q8JPM2_9HEPC	Q8jpm2 hepatitis c
1011	80	4.6	815	2	Q41S53_WHEAT	Q41s53 triticum ae	1084	79.5	4.6	750	2	Q41103_PHAVU	Q41103 phaseolus v
1012	80	4.6	862	2	Q7N9C5_PHOLL	Q7n9c5 photorhabdu	1085	79.5	4.6	791	2	Q7XAL5_WHEAT	Q7xal5 triticum ae
1013	80	4.6	902	1	FTFHD_PONPY	Q5rfm9 pongo pygma	1086	79.5	4.6	796	2	Q7XAL6_AEGTA	Q7xal6 aegilops ta
1014	80	4.6	946	2	Q96163_PLAP7	Q96163 plasmodium	1087	79.5	4.6	822	2	Q6PAE2_XENLA	Q6pae2 xenopus lae
1015	80	4.6	955	2	Q8A654_BACTN	Q8a654 bacteroides	1088	79.5	4.6	867	2	Q9A3S5_CAUCR	Q9a3s5 caulobacter
1016	80	4.6	1016	2	Q91779_XENLA	Q91779 xenopus lae	1089	79.5	4.6	922	2	Q5GVY2_XANOR	Q5gvv2 xanthomonas
1017	80	4.6	1258	2	Q8AW11_BRARE	Q8aw11 brachydanio	1090	79.5	4.6	946	2	Q5TUD3_HUMAN	Q5tfu3 homo sapien
1018	80	4.6	1306	2	Q93N36_PANAN	Q93n36 pantoea ana	1091	79.5	4.6	986	2	F93416_ORYSA	Q5t0u6 mus musculu
1019	80	4.6	1519	2	Q48237_HELUM	Q48237 helicobacte	1092	79.5	4.6	987	2	Q5TUD8_HUMAN	Q5t0u8 homo sapien
1020	80	4.6	1519	2	Q4PQ06_9HEPC	Q4pq06 hepatitis c	1093	79.5	4.6	988	2	O64454_ORYSA	Q64454 oryza sativ
1021	80	4.6	1641	2	Q5LJZ2_DROME	Q5ljz2 drosophila c	1094	79.5	4.6	1004	2	Q4LES3_HUMAN	Q4les3 homo sapien
1022	80	4.6	1646	2	Q4PQU2_9HEPC	Q4pqu2 hepatitis c	1095	79.5	4.6	1055	1	EPHE2_HUMAN	Q29323 homo sapien
1023	80	4.6	1694	2	Q8SA88_MAIZE	Q8sa88 zea mays (m	1096	79.5	4.6	1055	2	Q5TUD7_HUMAN	Q5t0u7 homo sapien
1024	80	4.6	1746	1	TENA_PIG	Q29116 sus scrofa (m	1097	79.5	4.6	1136	2	Q8K2V0_MOUSE	Q8k2v0 mus musculu
1025	80	4.6	1844	2	Q4FYM5_LEIMA	Q4fym5 leishmania	1098	79.5	4.6	1136	2	Q8C109_MOUSE	Q8c109 mus musculu
1026	80	4.6	1880	2	Q9DKW2_9CALI	Q9dkw2 walrus cali	1099	79.5	4.6	1136	2	Q5XKE0_MOUSE	Q5xke0 mus musculu
1027	80	4.6	3010	2	P90195_9HEPC	P90195 hepatitis c	1100	79.5	4.6	1175	2	Q9SWE0_MAIZE	Q9swe0 zea mays (m
1028	80	4.6	3010	2	Q9J3I1_9HEPC	Q9j3i1 hepatitis c	1101	79.5	4.6	1196	1	AMTB_PAEPO	P21543 paenibacill
1029	80	4.6	3586	2	Q7OKJ6_BACAM	Q7okj6 bacillus am	1102	79.5	4.6	1224	2	Q7T024_BRARE	Q7t024 brachydanio
1030	80	4.6	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila	1103	79.5	4.6	1323	2	Q8Y1G6_RALSO	Q8y1g6 raletonia s
1031	80	4.6	3843	2	Q9VU94_DROME	Q9vu94 drosophila	1104	79.5	4.6	1324	2	Q6AT13_BACPR	Q6at13 bacteroides
1032	79.5	4.6	200	2	Q70603_RAT	Q70603 rattus norv	1105	79.5	4.6	1389	2	Q4GSG3_TETNG	Q4gsg3 tetraodon n
1033	79.5	4.6	237	2	Q31175_NEIME	Q31175 neisseria m	1106	79.5	4.6	1644	2	Q4PQT1_9HEPC	Q4pqt1 hepatitis c
1034	79.5	4.6	241	2	Q9AE80_NEIME	Q9ae80 neisseria m	1107	79.5	4.6	1955	2	Q780A7_NEUCR	Q780a7 neurospora
1035	79.5	4.6	241	2	O07273_NEIME	O07273 neisseria m	1108	79.5	4.6	2236	1	PYR1_DROME	P05990 drosophila
1036	79.5	4.6	241	2	O07274_NEIME	O07274 neisseria m	1109	79.5	4.6	2489	2	Q16744_HUMAN	Q16744 homo sapien
1037	79.5	4.6	241	2	O07912_NEIME	O07912 neisseria m	1110	79.5	4.6	2761	2	Q18447_CAEL	Q18447 caenorhabdi
1038	79.5	4.6	254	2	Q9MS16_9FOAL	Q9ms16 piptatherum	1111	79.5	4.6	3011	2	Q9EL58_9HEPC	Q9el58 hepatitis c
1039	79.5	4.6	255	2	Q8PHU4_XANAC	Q8phu4 xanthomonas	1112	79.5	4.6	3013	2	Q9QIX9_9HEPC	Q9qix9 hepatitis c
1040	79.5	4.6	270	2	Q9RQV4_NEIME	Q9rqv4 neisseria m	1113	79.5	4.6	3412	2	Q7N1Z0_PHOLL	Q7n1z0 photorhabdu
1041	79.5	4.6	284	2	Q5TPH3_ANOGA	Q5tp3 anopheles g	1114	79.5	4.6	3531	2	Q7NNB1_GLOVI	Q7nnb1 gloeobacter
1042	79.5	4.6	301	2	Q7SZ01_XENLA	Q7sz01 xenopus lae	1115	79	4.5	323	2	Q5XWV2_GLOIX	Q5xwv2 gluconobact
1043	79.5	4.6	323	2	Q29041_PIG	Q29041 sus scrofa	1116	79	4.5	338	2	Q7XKL3_XENLA	Q7xkl3 xenopus lae
1044	79.5	4.6	326	2	Q9G51_9HEPC	Q9g51 hepatitis c	1117	79	4.5	343	2	Q8UUS7_9GGBI	Q8uus7 bostrychus
1045	79.5	4.6	329	2	Q6DIX5_XENTR	Q6dix5 xenopus tro	1118	79	4.5	371	2	Q8UUS7_9GGBI	Q8uus7 bostrychus
1046	79.5	4.6	335	1	FCN1_RAT	Q5m8b4 rattus norv	1119	79	4.5	372	2	Q8UUS7_9GGBI	Q8uus7 bostrychus
1047	79.5	4.6	335	1	FCN1_RAT	P11218 urtica dioi	1120	79	4.5	375	2	Q63YZ9_BURPS	Q63yz9 burkholderi
1048	79.5	4.6	372	1	AGI_URTDI	Q5y17 urtica dioi	1121	79	4.5	375	2	Q62GH0_BURMA	Q62gh0 burkholderi
1049	79.5	4.6	372	1	AGI_URTDI	Q5y17 urtica dioi	1122	79	4.5	405	2	Q4S6P4_TETNG	Q4s6p4 tetraodon n
1050	79.5	4.6	388	2	Q9SVR1_URTDI	Q9svr1 caenorhabdi	1123	79	4.5	414	1	NAS26_CAEL	Q22710 caenorhabdi
1051	79.5	4.6	388	2	Q9U307_CAEL	Q9u307 caenorhabdi	1124	79	4.5	431	2	Q86H05_BIOGL	Q86h05 biophalari
1052	79.5	4.6	426	2	Q4P8N6_USTMA	Q4p8n6 ustilago ma	1125	79	4.5	448	2	Q8DMZ4_STRR6	Q8dmz4 streptococ
1053	79.5	4.6	426	2	Q5XWV5_9HEPC	Q5xwv5 hepatitis c	1126	79	4.5	456	2	Q6AA53_PROAC	Q6aa53 propionibac



1127	79	4.5	466	2	Q81QK6_BACAN	Q81qk6 bacillus an
1128	79	4.5	490	2	Q4W8M3_9BACI	Q4w8m3 bacillus sp
1129	79	4.5	507	1	ALDH_STRCO	Qrjz6 streptomyc
1130	79	4.5	513	2	Q5CXK6_CRYPV	Q5cxr6 cryptospori
1131	79	4.5	519	2	Q9COT8_9SPHI	Q9crt8 cytophaga s
1132	79	4.5	531	2	Q97T17_CLOBH	Q97t17 clostridium
1133	79	4.5	535	2	Q8PXS1_METWA	Q8pxs1 methanosarc
1134	79	4.5	544	2	F74655_SYNY3	F74655 synchocyst
1135	79	4.5	551	2	Q4QNR4_HAB18	Q4qnr4 haemophilus
1136	79	4.5	555	2	Q61BQ7_ORYSA	Q6ieq7 oryza sativ
1137	79	4.5	565	2	Q8JUU5_9INFA	Q8juu5 influenza a
1138	79	4.5	566	2	Q8UWT1_9INFA	Q8uwt1 influenza a
1139	79	4.5	605	2	Q8S4W8_MAIZE	Q8s4w8 zea mays (m
1140	79	4.5	605	2	Q9FVF0_FRAAN	Q9fvf0 fragaria an
1141	79	4.5	606	2	Q8S4W9_MAIZE	Q8s4w9 zea mays (m
1142	79	4.5	625	1	TNR11_MOUSE	Q15305 mus musculu
1143	79	4.5	642	2	Q5BGY6_EMENI	Q5bgv6 aspergillus
1144	79	4.5	646	2	Q6ZN80_HUMAN	Q6zn80 homo sapien
1145	79	4.5	649	2	Q8YD80_BRUME	Q8yd80 bruceella me
1146	79	4.5	676	2	Q579L1_BRUAB	Q579l1 bruceella ab
1147	79	4.5	676	2	Q8FV51_BRUSU	Q8fvs1 bruceella su
1148	79	4.5	689	2	Q5LDX1_BACFN	Q5ldx1 bacteroides
1149	79	4.5	689	2	Q64V15_BACFR	Q64v15 bacteroides
1150	79	4.5	701	2	Q9T2A4_9POLA	Q9t2a4 alvimia gra
1151	79	4.5	702	2	Q9T2A1_OTAAC	Q9t2a1 oatea acum
1152	79	4.5	730	2	Q4XEX1_PLACH	Q4xex1 plasmodium
1153	79	4.5	747	2	Q98L70_RHILO	Q98l70 rhizobium l
1154	79	4.5	759	2	Q51NS3_MAGGR	Q5lns3 magnaporthe
1155	79	4.5	776	2	Q18696_CAEEL	Q18696 caenorhabdi
1156	79	4.5	835	2	Q99PX3_ECOLI	Q99px3 escherichia
1157	79	4.5	874	2	Q4UPV5_THEAN	Q4ufv5 theileria a
1158	79	4.5	902	2	Q53HP5_HUMAN	Q53hp5 homo sapien
1159	79	4.5	919	1	HEX_ADE12	P19900 human adeno
1160	79	4.5	971	2	Q9ZE42_RICPR	Q9ze42 ricettsia
1161	79	4.5	1374	2	Q6FPQ7_CANGA	Q6fpq7 candida gla
1162	79	4.5	1472	2	Q87B49_XYLFT	Q87b49 xylella fas
1163	79	4.5	1480	2	Q4TU93_RAT	Q4tu93 rattus norv
1164	79	4.5	1644	2	Q4PQ85_9HEPC	Q4pq85 hepatitis c
1165	79	4.5	1644	2	Q4PQ87_9HEPC	Q4pq87 hepatitis c
1166	79	4.5	2326	2	Q6BRQ7_DEBHA	Q6brq7 debaryomyce
1167	78.5	4.5	300	1	MRAW_CHLTR	Q84274 chlamydia t
1168	78.5	4.5	302	1	MRAW_CHLMU	Q84274 chlamydia m
1169	78.5	4.5	307	2	Q28703_RABIT	Q28703 cryptotaglus
1170	78.5	4.5	308	2	Q7QHK9_ANOGA	Q7qhk9 anopheles g
1171	78.5	4.5	312	2	Q62S50_CARBR	Q62s50 caenorhabdi
1172	78.5	4.5	312	2	Q5R5B2_PONPY	Q5r5b2 pongo pygma
1173	78.5	4.5	326	2	Q980T5_9HEPC	Q980t5 hepatitis c
1174	78.5	4.5	326	2	Q98V73_9HEPC	Q98v73 hepatitis c
1175	78.5	4.5	354	2	Q5ZK00_CHICK	Q5zk00 gallus gall
1176	78.5	4.5	360	2	Q68DD1_HUMAN	Q68dd1 homo sapien
1177	78.5	4.5	368	2	Q4IXP0_AZOVI	Q4ixp0 azotobacter
1178	78.5	4.5	372	2	Q7ZVP2_BRARE	Q7zvf2 brachydanio
1179	78.5	4.5	380	2	Q9F0R8_LYCES	Q9fur8 lycopersico
1180	78.5	4.5	387	2	Q18546_BIOGL	Q18546 biophalari
1181	78.5	4.5	394	2	Q9W6E6_9TELE	Q9w6e6 opasunus bet
1182	78.5	4.5	403	2	Q6DDK1_XENLA	Q6ddk1 xenopus lae
1183	78.5	4.5	409	2	Q9SP05_LYCES	Q9sp05 lycopersico
1184	78.5	4.5	412	2	Q9Z0R5_ARATH	Q9zqr5 arabidopsis
1185	78.5	4.5	414	2	Q749U8_GEOSL	Q749u8 geobacter s
1186	78.5	4.5	423	2	Q721Z8_DICDI	Q721z8 dictyostell
1187	78.5	4.5	426	2	Q5XMM4_9HEPC	Q5xmm4 hepatitis c
1188	78.5	4.5	426	2	Q5XMM6_9HEPC	Q5xmm6 hepatitis c
1189	78.5	4.5	426	2	Q5XMT0_9HEPC	Q5xmt0 hepatitis c
1190	78.5	4.5	426	2	Q5XMU2_9HEPC	Q5xmu2 hepatitis c
1191	78.5	4.5	426	2	Q5XNA4_9HEPC	Q5xna4 hepatitis c
1192	78.5	4.5	426	2	Q5XNA7_9HEPC	Q5xna7 hepatitis c
1193	78.5	4.5	426	2	Q5XN85_9HEPC	Q5xn85 hepatitis c
1194	78.5	4.5	426	2	Q5XNA0_9HEPC	Q5xna0 hepatitis c
1195	78.5	4.5	426	2	Q5XNA1_9HEPC	Q5xna1 hepatitis c
1196	78.5	4.5	426	2	Q5XNA2_9HEPC	Q5xna2 hepatitis c
1197	78.5	4.5	426	2	Q5XNC1_9HEPC	Q5xnc1 hepatitis c
1198	78.5	4.5	426	2	Q5XND1_9HEPC	Q5xnd1 hepatitis c
1199	78.5	4.5	426	2	Q5XNH3_9HEPC	Q5xnh3 hepatitis c

1200	78.5	4.5	426	2	Q5XNH6_9HEPC	Q5xnh6 hepatitis c
1201	78.5	4.5	440	2	Q8W546_WHEAT	Q8w546 triticum ae
1202	78.5	4.5	453	2	Q526H2_MAGGR	Q526h2 magnaporthe
1203	78.5	4.5	466	2	Q82M96_STRAW	Q82m96 streptomyc
1204	78.5	4.5	473	2	Q5M815_XENTR	Q5m815 xenopus chr
1205	78.5	4.5	479	2	Q8GN31_ERWCH	Q8gn31 erwania tho
1206	78.5	4.5	482	1	COBA1_RAT	P20909 rattus norv
1207	78.5	4.5	491	2	Q6CMT5_KJULA	Q6cm5 kluyveromyc
1208	78.5	4.5	491	2	Q9F012_PSECL	Q9f012 pseudomonas
1209	78.5	4.5	494	2	Q77839_9VIRU	Q7t839 glytapanate
1210	78.5	4.5	509	2	Q8WS99_9ECHI	Q8ws99 glytaster t
1211	78.5	4.5	531	2	Q8G7R4_BIFLO	Q8g7r4 bifidobacte
1212	78.5	4.5	551	2	Q8WP18_MACFA	Q8wp18 macaca fasc
1213	78.5	4.5	566	2	Q82752_9ORTO	Q82752 unidentified
1214	78.5	4.5	566	2	Q82774_9INFA	Q82774 influenza a
1215	78.5	4.5	568	2	Q5BJV4_RAT	Q5bjv4 rattus norv
1216	78.5	4.5	576	2	Q4KP42_9HEPC	Q4kp42 hepatitis c
1217	78.5	4.5	622	2	Q6D8P1_ERWCT	Q6d8p1 erwania car
1218	78.5	4.5	626	2	P92990_ARATH	P92990 arabidopsis
1219	78.5	4.5	655	2	Q8WQX8_BIOGL	Q8wxq8 biophalari
1220	78.5	4.5	661	2	Q8A103_BACTN	Q8a103 bacteroides
1221	78.5	4.5	673	2	Q4RKJ4_TETNG	Q4rkj4 tetraodon n
1222	78.5	4.5	698	1	YMCA_ECOLI	P75882 escherichia
1223	78.5	4.5	698	2	Q48900_MAIZE	Q48900 zea mays (m
1224	78.5	4.5	764	2	Q8VNM0_WHEAT	Q8vnm0 triticum ae
1225	78.5	4.5	764	2	Q68881_PSEAE	Q68881 pseudomonas
1226	78.5	4.5	764	2	Q9HV88_PSEAE	Q9hv88 pseudomonas
1227	78.5	4.5	770	1	GLGB_STNY3	P52981 synchocyst
1228	78.5	4.5	780	2	Q9XAL9_STRCO	Q9xal9 streptomyc
1229	78.5	4.5	791	2	Q8W547_WHEAT	Q8w547 triticum ae
1230	78.5	4.5	804	2	Q6ZQE3_MOUSE	Q6zqe3 mus musculu
1231	78.5	4.5	823	2	Q6LR67_PHOPR	Q6lr67 photobacter
1232	78.5	4.5	837	2	Q9A3Q6_CAUCR	Q9a3q6 caulobacter
1233	78.5	4.5	853	2	Q61PK3_HUMAN	Q6ipk3 homo sapien
1234	78.5	4.5	870	2	Q6FC24_ACIAD	Q6fc24 acinetobact
1235	78.5	4.5	883	2	Q4XEH8_PLACH	Q4xeh8 plasmodium
1236	78.5	4.5	900	1	MANBA_CAEEL	Q93324 caenorhabdi
1237	78.5	4.5	914	2	Q29964_ARCFU	Q29964 archaeoglob
1238	78.5	4.5	922	2	O8PLC0_XANCP	Q8plc0 xanthomonas
1239	78.5	4.5	989	2	Q9FWN6_CHICK	Q9fwn6 gallus gall
1240	78.5	4.5	990	2	Q8LNN7_ORYSA	Q8lnn7 oryza sativ
1241	78.5	4.5	993	2	Q9L036_STRCO	Q9l036 streptomyc
1242	78.5	4.5	1005	1	TARP1_CHLTR	Q84462 chlamydia t
1243	78.5	4.5	1014	2	Q8WP17_MACFA	Q8wp17 macaca fasc
1244	78.5	4.5	1015	2	Q4UNG2_XANCP	Q4ung2 xanthomonas
1245	78.5	4.5	1015	2	Q8P7N8_XANCP	Q8p7n8 xanthomonas
1246	78.5	4.5	1020	2	Q7Q204_ANOGA	Q7q204 anopheles g
1247	78.5	4.5	1137	1	BCSC_ECO57	Q8x5m0 escherichia
1248	78.5	4.5	1139	1	HMW1_MYCGE	Q49413 mycoplasma
1249	78.5	4.5	1191	2	Q4S4D3_TETNG	Q4s4d3 tetraodon n
1250	78.5	4.5	1234	2	Q77285_DROME	Q77285 drosophila
1251	78.5	4.5	1234	2	Q9W0B8_DROME	Q9w0b8 drosophila
1252	78.5	4.5	1248	1	TPP2_RAT	Q64560 rattus norv
1253	78.5	4.5	1249	2	Q5D072_MOUSE	Q5d072 mus musculu
1254	78.5	4.5	1261	1	TPP2_MOUSE	Q64514 mus musculu
1255	78.5	4.5	1363	2	Q8BZ47_MOUSE	Q8bz47 mus musculu
1256	78.5	4.5	1395	2	Q9AISO_9STAP	Q9ais0 staphylococ
1257	78.5	4.5	1436	1	WC11_BOVIN	P30205 bos taurus
1258	78.5	4.5	1506	2	Q54U77_DICDI	Q54u77 dictyostell
1259	78.5	4.5	1549	2	Q6MIW7_BDEBA	Q6miw7 bdellovibri
1260	78.5	4.5	1595	2	Q6MNK4_BDEBA	Q6mnk4 bdellovibri
1261	78.5	4.5	1766	2	Q8AW45_BRARE	Q8aw45 brachydanio
1262	78.5	4.5	1838	2	Q15094_HUMAN	Q15094 homo sapien
1263	78.5	4.5	2014	2	Q29530_PANTR	Q29530 pan troglod
1264	78.5	4.5	2221	1	F3CBZ3_BACCI	Q73bz3 bacillus ce
1265	78.5	4.5	2481	1	FINC_XENLA	Q91740 xenopus lae
1266	78.5	4.5	2481	2	Q6QA05_XENLA	Q6qa05 xenopus lae
1267	78.5	4.5	2653	2	Q25253_LUCCT	Q25253 lucilia cup
1268	78.5	4.5	417	2	Q582D2_9TRYP	Q582d2 trypanosoma
1269	78	4.5	176	2	Q6EXK3_BIOGL	Q6exk3 biophalari
1270	78	4.5	267	2	Q6EXK3_RAT	Q6x583 rattus norv
1271	78	4.5	310	2	Q6CYZ3_ERWCT	Q6cyz3 erwania car
1272	78	4.5	317	2	Q93WY7_TOBAC	Q93wy7 nicotiana t

1273	78	4.5	318	2	Q95YH3_9EUKA	Q95yh3 pseudotrich	1346	77.5	4.4	257	2	Q5YB91_9SPHN	Q5yb91 spingomona
1274	78	4.5	321	2	Q6NJ01_CORDI	Q6nj01 corynebacte	1347	77.5	4.4	271	2	Q7UXU2_RHOBA	Q7uxu2 rhodopirell
1275	78	4.5	344	2	Q8MNB1_DICDI	Q8mbn1 dictyosteli	1348	77.5	4.4	306	2	Q5FVU9_XENTR	Q5fvu9 xenopus tro
1276	78	4.5	349	2	Q04676_HORVU	Q04676 hordeum vul	1349	77.5	4.4	315	2	Q7MUB0_PORGI	Q7mub0 porphyromon
1277	78	4.5	351	2	Q93PW0_PARPEN	Q93pw0 paracoccus	1350	77.5	4.4	324	2	Q7FEW1_NICSY	Q7few1 nicotiana s
1278	78	4.5	360	2	Q67Q12_SYMTH	Q67q12 symbiobacte	1351	77.5	4.4	326	2	Q9WG50_9HEPC	Q9wg50 hepatitis c
1279	78	4.5	371	2	Q8UUS6_GOBI	Q8uus6 bostrychus	1352	77.5	4.4	332	2	Q9WG54_9HEPC	Q9wg54 hepatitis c
1280	78	4.5	387	2	Q6E202_RIEAN	Q6e202 riemerella	1353	77.5	4.4	334	2	Q6OLK8_CAEBR	Q6olk8 caenorhabdi
1281	78	4.5	396	2	Q88G25_FSEPK	Q88g25 pseudomonas	1354	77.5	4.4	405	1	ANGL4_RAT	Q6ema8 caenorhabdi
1282	78	4.5	397	2	Q9F250_ARATH	Q9f250 arabisopsis	1355	77.5	4.4	410	1	ANGL4_MOUSE	Q6ema8 rat mus musculu
1283	78	4.5	404	2	Q22791_ARATH	Q22791 arabisopsis	1356	77.5	4.4	410	1	ANGL4_MOUSE	Q6ema8 mus musculu
1284	78	4.5	423	2	Q8GY81_ARATH	Q8gy81 arabisopsis	1357	77.5	4.4	423	2	Q55FW5_DICDI	Q55fw5 dictyosteli
1285	78	4.5	453	2	Q6MR90_BDEBA	Q6mr90 bdellovibri	1358	77.5	4.4	426	2	Q5XNV9_9HEPC	Q5xmv9 hepatitis c
1286	78	4.5	497	2	Q6BMV1_DEBHA	Q6bmvi debaryomyce	1359	77.5	4.4	426	2	Q5XNV9_9HEPC	Q5xmv9 hepatitis c
1287	78	4.5	507	2	Q6QD15_9RHAB	Q6qd15 viral hemor	1360	77.5	4.4	426	2	Q5XNM6_9HEPC	Q5xnm6 hepatitis c
1288	78	4.5	511	2	Q60637_MOUSE	Q60637 mus musculu	1361	77.5	4.4	426	2	Q5XNM6_9HEPC	Q5xnm6 hepatitis c
1289	78	4.5	544	2	Q9NUL8_HUMAN	Q9nul8 homo sapien	1362	77.5	4.4	426	2	Q5XNM6_9HEPC	Q5xnm6 hepatitis c
1290	78	4.5	559	2	Q6DX25_9INFA	Q6dx25 influenza a	1363	77.5	4.4	426	2	Q5XNM6_9HEPC	Q5xnm6 hepatitis c
1291	78	4.5	571	2	Q9EY44_CELUD	Q9ey44 cellulomona	1364	77.5	4.4	456	2	Q8VZ33_ARATH	Q8vz33 arabidopsis
1292	78	4.5	584	2	Q640P8_MOUSE	Q640p8 mus musculu	1365	77.5	4.4	456	2	Q8VZ33_ARATH	Q8vz33 arabidopsis
1293	78	4.5	584	2	Q81118_WHEAT	Q81118 triticum ae	1366	77.5	4.4	464	2	Q7UXP2_RHOBA	Q7uxp2 rhodopirell
1294	78	4.5	586	2	Q8BJW6_MOUSE	Q8bjw6 m mus muscu	1367	77.5	4.4	464	2	Q7UXP2_RHOBA	Q7uxp2 rhodopirell
1295	78	4.5	623	2	Q7SZG1_FUGRU	Q7szg1 fugu rubrip	1368	77.5	4.4	464	2	Q7UXP2_RHOBA	Q7uxp2 rhodopirell
1296	78	4.5	625	2	Q7Z867_USTMA	Q7z867 ustilago ma	1369	77.5	4.4	472	2	Q7XD15_ORYSA	Q7xd15 oryza sativ
1297	78	4.5	635	2	Q4PG50_USTMA	Q4pg50 ustilago ma	1370	77.5	4.4	491	1	ANGL4_HUMAN	Q673v5 solemya vel
1298	78	4.5	641	2	Q4LV49_9BURK	Q4lv49 burkholderi	1371	77.5	4.4	491	1	ANGL4_HUMAN	Q673v5 solemya vel
1299	78	4.5	647	2	Q8ALV0_BACTN	Q8alv0 bacteroides	1372	77.5	4.4	559	2	Q84BN2_9CELL	Q84bn2 cellulomona
1300	78	4.5	666	1	NEPU1_THEVU	Q5aak0 bacteroides	1373	77.5	4.4	570	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
1301	78	4.5	675	2	Q412V4_GIBZE	Q412v4 gibberella	1374	77.5	4.4	570	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
1302	78	4.5	706	2	Q32045_9POAL	Q32045 cephalostac	1375	77.5	4.4	580	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
1303	78	4.5	730	2	Q898P2_CLOTE	Q898p2 clostridium	1376	77.5	4.4	586	2	Q6U9U2_9CAUD	Q6u9u2 bacterioph
1304	78	4.5	743	2	Q5H0V1_XANOR	Q5h0v1 xanthomonas	1377	77.5	4.4	597	1	DFA3_SYNY3	Q4x079 aspergillus
1305	78	4.5	762	1	E13B_TRIHA	P53626 trichoderma	1378	77.5	4.4	606	2	Q6ZAZ7_ORYSA	Q6zaz7 oryza sativ
1306	78	4.5	771	2	Q8SD31_9CAUD	Q8sd31 pseudomonas	1379	77.5	4.4	627	2	Q6ZAZ7_ORYSA	Q6zaz7 oryza sativ
1307	78	4.5	785	2	Q5DIW0_PSEAE	Q5diw0 pseudomonas	1380	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1308	78	4.5	786	2	Q4LU26_9BURK	Q4lu26 burkholderi	1381	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1309	78	4.5	795	2	Q9NV89_HUMAN	Q9nv89 homo sapien	1382	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1310	78	4.5	795	2	Q9UF53_HUMAN	Q9uf53 homo sapien	1383	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1311	78	4.5	801	1	PISK1_ORYSA	Q6x442 oryza sativ	1384	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1312	78	4.5	811	2	Q5KAV3_CRYNE	Q5kav3 cryptococcu	1385	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1313	78	4.5	811	2	Q5SKL8_CRYNE	Q5skl8 cryptococcu	1386	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1314	78	4.5	815	1	FPVA_PSEAE	P48632 pseudomonas	1387	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1315	78	4.5	829	2	Q9ZTB6_HORVU	Q9ztb6 hordeum vul	1388	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1316	78	4.5	843	2	Q5SVV3_CRYNE	Q5svv3 cryptococcu	1389	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1317	78	4.5	843	2	Q5KOD5_CRYNE	Q5kod5 cryptococcu	1390	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1318	78	4.5	918	2	Q61DS4_CAEBR	Q61ds4 caenorhabdi	1391	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1319	78	4.5	919	2	Q6BUI9_DEBHA	Q6bui9 debaryomyce	1392	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1320	78	4.5	931	2	Q4F8U9_PLACH	Q4f8u9 plasmodium	1393	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1321	78	4.5	942	1	AMPE_FIG	Q95334 sus scrofa	1394	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1322	78	4.5	962	2	Q4K4X8_PSEF5	Q4k4x8 pseudomonas	1395	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1323	78	4.5	986	1	GUNZ_GLOS	P23659 clostridium	1396	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1324	78	4.5	1015	2	Q6NLL2_9MICC	Q6nll2 arthrobacte	1397	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1325	78	4.5	1060	2	Q64YL2_BACPR	Q64yl2 bacteroides	1398	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1326	78	4.5	1083	2	Q5ICE3_ENTHI	Q5ice3 entamoeba h	1399	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1327	78	4.5	1206	2	Q869X8_DICDI	Q869x8 dictyosteli	1400	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1328	78	4.5	1236	2	Q4P320_USTMA	Q4p320 ustilago ma	1401	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1329	78	4.5	1242	2	Q9PZX3_EBEV	Q9pzx3 eastern equ	1402	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1330	78	4.5	1303	2	Q76YAB_9CAUD	Q76yab bacterioph	1403	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1331	78	4.5	1454	2	Q69A94_LUME	Q69a94 leucostoc	1404	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1332	78	4.5	1623	2	Q4SAP8_TYING	Q4sap8 tetradodon n	1405	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1333	78	4.5	1902	2	Q9F878_COCOPO	Q9f878 coccidioid	1406	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1334	78	4.5	2261	2	Q9LXT9_ARATH	Q9lxt9 arabidopsis	1407	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1335	78	4.5	2261	2	Q61V05_CAEBR	Q61v05 caenorhabdi	1408	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1336	78	4.5	4370	2	Q4Q1Q2_LEIMA	Q4q1q2 leishmania	1409	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1337	77.5	4.4	152	2	Q9XSG8_PIG	Q9xsg8 sus scrofa	1410	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1338	77.5	4.4	178	2	Q7Q217_ANOGA	Q7q217 anopheles g	1411	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1339	77.5	4.4	187	2	Q92531_HUMAN	Q92531 homo sapien	1412	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1340	77.5	4.4	189	1	ICFA_MANSE	P00305 manduca sex	1413	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1341	77.5	4.4	197	2	Q8F122_LEPIN	Q8f122 leptospira	1414	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1342	77.5	4.4	206	1	ICYB_MANSE	Q00630 manduca sex	1415	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1343	77.5	4.4	220	2	Q9H0L1_WHEAT	Q9h0l1 triticum ae	1416	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1344	77.5	4.4	237	2	Q69357_RHOER	Q69357 rhodococcus	1417	77.5	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ
1345	77.5	4.4	250	2	Q3FMN8_XENLA	Q3fmn8 xenopus lae	1418	77	4.4	635	1	SVT_XYLF	Q6zaz7 oryza sativ

1419	77	4.4	274	2	Q9NAH7 CAEBL	Q9nah7 caenorhabdi	1492	77	4.4	917	2	Q9FLT8 ARATH	Q9flt8 arabidopsis
1420	77	4.4	286	2	Q9KEF2_BACHD	Q9kef2 bacillus ha	1493	77	4.4	1016	2	Q4S3H9_TETNG	Q4s3h9 tetraodon n
1421	77	4.4	290	2	Q8QNN5_9PHYC	Q8qnn5 ectocarpus	1494	77	4.4	1090	2	Q8A812_BACTN	Q8a812 bacteroides
1422	77	4.4	319	2	Q7WIL3_BORPA	Q7wil3 bordetella	1495	77	4.4	1110	2	Q8A894_BACTN	Q8a894 bacteroides
1423	77	4.4	319	2	Q7WPK4_BORER	Q7wpk4 bordetella	1496	77	4.4	1214	2	Q88193_9CALI	Q88193 san miguel
1424	77	4.4	327	2	Q98V50_9HEPC	Q98v50 hepatitis c	1497	77	4.4	1245	2	Q9Y7V5_TRIHA	Q9y7v5 trichoderma
1425	77	4.4	328	2	Q9LSI5_ARATH	Q9lsi5 arabidopsis	1498	77	4.4	1358	1	PUR4_YEAST	P38972 saccharomyc
1426	77	4.4	332	2	Q6AFQ1_LEIYX	Q6afq1 leifsonia x	1499	77	4.4	1632	2	Q8TI41_METAC	Q8ti41 methanosarc
1427	77	4.4	344	1	ANGL7_BOVIN	O5ea66 bos taurus	1500	77	4.4	1809	2	Q8T398_CIOIN	Q8t398 ciona intes
1428	77	4.4	361	2	Q5K4M1_CRAGI	O5k4m1 crasostrea							
1429	77	4.4	390	2	Q4LMR3_9BURK	Q4lmr3 burkholderi							
1430	77	4.4	390	2	Q9K7M8_BACHD	Q9k7m8 bacillus ha							
1431	77	4.4	397	2	Q9S3W0_BACFR	Q9s3w0 bacteroides							
1432	77	4.4	399	2	Q7Z664_HUMAN	Q7z664 homo sapien							
1433	77	4.4	405	1	ENTM_BACFR	P54355 bacteroides							
1434	77	4.4	412	2	Q7UA80_SYNPX	Q7ua80 synchococc							
1435	77	4.4	418	2	Q8YVQ8_ANASP	Q8yvq8 anabaena sp							
1436	77	4.4	437	2	Q53Y18_HUMAN	Q53y18 homo sapien							
1437	77	4.4	441	2	Q4K435_PSEPS	Q4k435 pseudomonas							
1438	77	4.4	453	1	FIBG_HUMAN	P02679 homo sapien							
1439	77	4.4	459	1	GUNI_TRIRE	P07981 trichoderma							
1440	77	4.4	459	2	O5BM55_TRIRE	O5bme5 trichoderma							
1441	77	4.4	460	1	GUNC_CLOCE	P37899 clostridium							
1442	77	4.4	461	1	HDAL_CAEBL	Q17695 caenorhabdi							
1443	77	4.4	464	2	Q7MAV4_TRIVI	Q7mav4 trichoderma							
1444	77	4.4	471	2	Q83X15_STRRO	Q83x15 streptomyce							
1445	77	4.4	492	2	O5MQD6_9INFA	O5mqd6 influenza a							
1446	77	4.4	505	2	Q6VQO7_9RHAB	O6vqo7 infectious							
1447	77	4.4	508	2	Q778K0_9RHAB	Q778k0 hirame rhab							
1448	77	4.4	508	2	Q82693_9RHAB	Q82693 infectious							
1449	77	4.4	508	2	Q82705_9RHAB	Q82705 infectious							
1450	77	4.4	515	2	Q7UK62_RHOBA	Q7uk62 rhodopirell							
1451	77	4.4	523	1	Q8A0A5_BACTN	Q8a0a5 bacteroides							
1452	77	4.4	551	1	Y275_HA8IN	P43975 haemophilus							
1453	77	4.4	557	2	Q6DXD7_9INFA	Q6dxd7 influenza a							
1454	77	4.4	557	2	Q6DXF2_9INFA	Q6dxkf2 influenza a							
1455	77	4.4	562	2	Q6DXO9_9INFA	Q6dxo9 influenza a							
1456	77	4.4	564	1	HEWA_IADAL	P03443 influenza a							
1457	77	4.4	565	2	Q9ZB54_9BURK	Q9zb54 alcaligenes							
1458	77	4.4	565	2	Q67010_9INFA	Q67010 influenza a							
1459	77	4.4	569	1	MALT_C9NAL	Q02751 candida alb							
1460	77	4.4	570	2	Q5ACH4_CANAL	Q5ach4 candida alb							
1461	77	4.4	577	1	ZP3R_RAT	Q578y4 gallus norv							
1462	77	4.4	586	2	Q5ZKC1_CHICK	Q5zkc1 gallus gall							
1463	77	4.4	588	2	Q5BN15_PETHY	Q5bn15 petunia hyb							
1464	77	4.4	604	2	Q67J86_SYMTH	Q67j86 symbiobacte							
1465	77	4.4	609	2	Q91776_XENLA	Q91776 xenopus lae							
1466	77	4.4	614	1	BTUB_SALPA	Q57h87 salmonella							
1467	77	4.4	614	1	BTUB_SALPA	Q5pk67 salmonella							
1468	77	4.4	614	1	BTUB_SALTY	Q82314 salmonella							
1469	77	4.4	614	1	BTUB_SALTY	P37409 salmonella							
1470	77	4.4	618	1	THRE_MOUSE	P19221 mus musculu							
1471	77	4.4	621	2	Q9C283_NEUCR	Q9c283 neurospora							
1472	77	4.4	627	2	Q9EUR5_STRPN	Q9eur5 streptococc							
1473	77	4.4	628	2	Q9S032_CAEBL	Q9s032 caenorhabdi							
1474	77	4.4	659	2	Q4KK22_PSEPF5	Q4kk22 pseudomonas							
1475	77	4.4	668	1	F13B_MOUSE	Q07968 mus musculu							
1476	77	4.4	681	2	Q41ZQ9_AZOVI	Q41zq9 azotobacter							
1477	77	4.4	702	2	Q9T296_9POAL	Q9t296 neurolepis							
1478	77	4.4	757	2	Q93DC1_9RHIZ	Q93dc1 agrobacteri							
1479	77	4.4	757	2	Q8UKF2_AGR75	Q8ukf2 agrobacteri							
1480	77	4.4	794	2	Q8C6C4_MOUSE	Q8c6c4 mus musculu							
1481	77	4.4	795	2	Q7D3R9_AGR75	Q7d3r9 agrobacteri							
1482	77	4.4	797	2	Q5H9R5_HUMAN	Q5h9r5 homo sapien							
1483	77	4.4	812	2	Q41VB3_AZOVI	Q41vb3 azotobacter							
1484	77	4.4	822	2	Q25021_HABEO	Q25021 haemonchus							
1485	77	4.4	823	2	Q4TG64_TETNG	Q4tg64 tetraodon n							
1486	77	4.4	827	2	Q8W0A1_ORYSA	Q8w0a1 oryza sativ							
1487	77	4.4	848	2	Q6VE86_PSESY	Q6ve86 pseudomonas							
1488	77	4.4	860	2	Q62308_MOUSE	Q62308 mus musculu							
1489	77	4.4	861	2	Q5SNL5_CRYNE	Q5snl5 cryptococcu							
1490	77	4.4	865	2	Q8Q072_METMA	Q8q072 methanosarc							
1491	77	4.4	866	1	YCBS_ECOLI	P75857 escherichia							

## ALIGNMENTS

## RESULT 1

## Q5IWS5 HUMAN

ID Q5IWS5 HUMAN PRELIMINARY; PRT; 313 AA.

AC Q5IWS5;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Intelectin 1 (Intelectin variant).

GN Name=ITIN1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Ovary;

RA Peavy T.R., Hedrick J.L.;

RT "Human homolog of the Xenopus laevis egg cortical granule lectin.";

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Adipose tissue;

RA Maruyama K., Sugano S.;

RT "Oligo-capping : a simple method to replace the cap structure of

RT eucaryotic mRNAs with oligoribonucleotides.";

RL Gene 138:171-174(1994).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Adipose tissue;

RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;

RT "Construction and characterization of a full length-enriched and a 5'-

RT end-enriched cDNA library.";

RL Gene 200:149-156(1997).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Adipose tissue;

RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,

RA Tanaka A., Yokoyama S.;

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY619691; AAU8047.1; -; mRNA.

DR EMBL; AK222533; BAD96253.1; -; mRNA.

SQ SEQUENCE 313 AA; 34977 MW; D82D4C173ED1B2EB CRC64;

Query Match 100.0%; Score 1747; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 3.1e-136;

Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQLSFLPLIATTTGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECSAFDGLYFLRT 60

Db 1 MNQLSFLPLIATTTGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECSAFDGLYFLRT 60

QY 61 ENGVIYQTCMDTSGGGGWTLVASVHENDMRGKCTVGDWSSQGSKADYPEDGNGWANY 120

Db 61 ENGVIYQTCMDTSGGGGWTLVASVHENDMRGKCTVGDWSSQGSKADYPEDGNGWANY 120

QY 121 NTFGSAEATSDDYKNPGYYDIOAKDLGIWHVPNKSPMQHWRNSSLRLRTDTGFIQTILG 180

Db 121 NTFGSAEATSDDYKNPGYYDIOAKDLGIWHVPNKSPMQHWRNSSLRLRTDTGFIQTILG 180

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QY 181 HNLFGIYKYPVKYGEKWTNDNGFVIVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 240
Db 181 HNLFGIYKYPVKYGEKWTNDNGFVIVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 240
QY 241 FNNRAANALCAGMRVTCNTEHHCICGGYFFPEASPOQCDGSGDFWGSYGTHVGYSS 300
Db 241 FNNRAANALCAGMRVTCNTEHHCICGGYFFPEASPOQCDGSGDFWGSYGTHVGYSS 300
QY 301 REITEAAVLLFYR 313
Db 301 REITEAAVLLFYR 313

RESULT 2
ID ITLN1 HUMAN STANDARD; PRT; 313 AA.
AC OSWAG; Q6YDJ3; Q9NP67;
DT 01-FEB-2005 (Rel. 46, Created)
DT 13-FEB-2005 (Rel. 46, Last sequence update)
DE Intelectin-1 precursor (Intestinal lactoferrin receptor)
DE (Galactofuranose binding lectin) [Endothelial lectin HL-1] (Omentin).
GN Name=ITLN1; Synonyms=INTL, ITLN, LFR; ORFNames=UNQ640/PRO1270;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 19-28, FUNCTION, SUBCELLULAR
RP LOCATION, TISSUE SPECIFICITY, SUBUNIT, N-GLYCOSYLATION, AND VARIANT
RP ASP-109
RC TISSUE=Placenta;
RX PubMed=11313366; DOI=10.1074/jbc.M103162200;
RA Teuji S., Uehori J., Matsumoto M., Suzuki Y., Matsuhisa A.,
RA Toyoshima K., Seya T.;
RT "Human intelectin is a novel soluble lectin that recognizes
RT galactofuranose in carbohydrate chains of bacterial cell wall."
RL J. Biol. Chem. 276:23456-23463 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE, GPI-ANCHOR, AND TISSUE SPECIFICITY.
RC TISSUE=Small intestine;
RX PubMed=11747454; DOI=10.1021/bi0155899;
RA Suzuki Y.A., Shin K., Loenneker B.;
RT "Molecular cloning and functional expression of a human intestinal
RT lactoferrin receptor."
RL Biochemistry 40:15771-15779 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC TISSUE=Small intestine;
RX PubMed=21096026; PubMed=11181563; DOI=10.1093/glycob/11.1.65;
RA Lee J.K., Schnee J., Pang M., Wolfert M., Baum L.G., Moremen K.W.,
RA Pierce M.;
RT "Human homologs of the Xenopus oocyte cortical granule lectin XI35."
RL Glycobiology 11:65-73 (2001).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANT PRO-313.
RX PubMed=14720597; DOI=10.1016/S1095-6433(03)00269-1;
RA Chang B.Y., Peavy T.R., Wardrip N.J., Hedrick J.L.;
RT "The Xenopus laevis cortical granule lectin: cDNA cloning,
RT developmental expression, and identification of the eglectin family of
RT lectins."
RL Comp. Biochem. Physiol. 137A:115-129 (2004).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Yang R.-Z., Shuldiner A.R., Gong D.-W.;
RT "Cloning of omentin, a new adipokine from human oment fat tissue."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Ebert L., Schick M., Neubert P., Schattten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway (TM) system entry
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RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robb E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RN Genome Res. 13:2265-2270 (2003).
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Adipose tissue;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa K.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togashi K., Ohtsuki T., Hara K., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Morioka Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu Y., Suzuki O.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heif F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., McKernan K.J., Muralthy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: May play a role in the defense system against  
CC microorganisms. May specifically recognize carbohydrate chains of  
CC pathogens and bacterial components containing galactofuranosyl  
CC residues, in a calcium-dependent manner. May be involved in iron  
CC metabolism.  
CC -!- SUBUNIT: Homotrimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC Also secreted.  
CC -!- TISSUE SPECIFICITY: Specifically expressed in the small intestine.  
CC Also found the heart, testis, colon, salivary gland, skeletal  
CC muscle, pancreas and thyroid; and to a lesser degree in the  
CC uterus, spleen, prostate, lymph node and thymus.  
CC -!- DEVELOPMENTAL STAGE: Found in fetal small intestine and thymus.  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
CC -!- CAUTION: The two mouse genes Itln1a and Itln1b are the paralogs of  
CC human ITLN1.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AB036706; BAA96094.1; -; mRNA.  
CC EMBL; AF271386; AAM20741.1; -; mRNA.  
CC EMBL; AY065972; AAL58073.1; -; mRNA.  
CC EMBL; AY157361; AAO17800.1; -; mRNA.  
CC EMBL; AY157362; AAO17801.1; -; mRNA.  
CC EMBL; AY549722; AAS49907.1; -; mRNA.  
CC EMBL; CR457224; CAG33505.1; -; mRNA.  
CC EMBL; AY358359; AAO88725.1; -; mRNA.  
CC EMBL; AK000029; BAA90893.1; -; mRNA.  
CC EMBL; BC020664; AAH20664.1; -; mRNA.  
CC EMBL; ENSG00000179914; Homo sapiens.  
CC HGNC; HGNC:18259; ITLN1.  
CC InterPro; IPR002181; Fibrinogen\_C.  
CC Pfam; PF00147; Fibrinogen\_C; 1.  
CC SMART; SM00186; FBG; 1.  
CC Direct protein sequencing: Glycoprotein; GPI-anchor; Lectin;  
KW Lipoprotein; Membrane; Polymorphism; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 298 Intelectin-1.  
FT PROPEP 299 313 Potential.  
FT DOMAIN 36 209 Fibrinogen C-terminal.  
FT LIPID 298 298 GPI-anchor amidated serine (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Probable).  
FT VARIANT 109 109 V -> D (in dbSNP:2274907).  
FT VARIANT 313 313 R -> P (in dbSNP:8144).  
FT SEQUENCE 313 AA; 34962 MW; 56219FE937FC802E CRC64;  
SQ  
Query Match 99.5%; Score 1738; DB 1; Length 313;  
Best Local Similarity 99.7%; Pred. No. 1.7e-135;  
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
DB 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
QY 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
DB 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
QY 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180  
DB 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180  
QY 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
DB 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
QY 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
DB 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
QY 301 REITEAAVLLFYR 313  
DB 301 REITEAAVLLFYR 313  
RESULT 4  
QSIWS4 HUMAN  
ID QSIWS4 HUMAN PRELIMINARY; PRT; 313 AA.  
AC QSIWS4.  
DT 10-MAY-2005 (Tremblrel. 30, Created)  
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
DE Intelectin 1.  
GN Name=ITLN1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Van Hellmond Z.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL354714; CAH72357.1; -; Genomic DNA.  
SQ SEQUENCE 313 AA; 34961 MW; 56219FE937FC802E CRC64;  
Query Match 99.5%; Score 1738; DB 2; Length 313;  
Best Local Similarity 99.7%; Pred. No. 1.7e-135;  
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
DB 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
QY 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
DB 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
QY 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180  
DB 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180

QY 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
DB 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
QY 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
DB 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
QY 301 REITEAAVLLFYR 313  
DB 301 REITEAAVLLFYR 313  
RESULT 3  
QSIWS4 HUMAN  
ID QSIWS4 HUMAN PRELIMINARY; PRT; 313 AA.  
AC QSIWS4.  
DT 01-FEB-2005 (Tremblrel. 29, Created)  
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)  
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)  
DE Intelectin 1 (Galactofuranose binding).  
GN Name=ITLN1; ORFNames=RP11-312J18.4-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Van Hellmond Z.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL354714; CAH72357.1; -; Genomic DNA.  
SQ SEQUENCE 313 AA; 34961 MW; 56219FE937FC802E CRC64;  
Query Match 99.5%; Score 1738; DB 2; Length 313;  
Best Local Similarity 99.7%; Pred. No. 1.7e-135;  
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
DB 1 MNQSLFLFLIATTRGWSSTDEANTYFKWTCSSPSLPRSCKEIKDECPSPDGLYFLRT 60  
QY 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
DB 61 ENGVIYQTCMDTSGGGWTLVAVSHENDMRGKCTVGDWSSQOQSKADYPGSGDNWANY 120  
QY 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180  
DB 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQTIG 180  
QY 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
DB 181 HNLFGIYOKYPVKYGEKWTNDGVPVIVVYDFGDAQKTASYSPYQOREFTAGFVQPRV 240  
QY 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
DB 241 FNNERAAALCAGMRVTGNTCEHHICIGGGYFPPEASPOCGDFSGDFSGDWSGYGTHVGYSS 300  
QY 301 REITEAAVLLFYR 313  
DB 301 REITEAAVLLFYR 313

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovary;  
 RA Peavy T.R., Hedrick J.L.;  
 RT "Human homolog of the Xenopus laevis egg cortical granule lectin.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY619592; AAU8048.1; -; mRNA.  
 SQ SEQUENCE 313 AA; 34902 MW; 55419PB937FC802E CRC64;

Query Match 99.2%; Score 1733; DB 2; Length 313;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-135;  
 Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNQLSFLFLIATTRGWSMTDEANTYFKETWCSSPSLPRSCKEIKDCPSAFDGLYFLRT 60  
 Db 1 MNQLSFLFLIATTRGWSMTDEANTYFKETWCSSPSLPRSCKEIKDCPSAFDGLYFLRT 60  
 QY 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANY 120  
 Db 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANY 120  
 QY 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPKNSPMQHWNSLLRYRTDTGFLQTLG 180  
 Db 121 NTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPKNSPMQHWNSLLRYRTDTGFLQTLG 180  
 QY 181 HNLFGIYQKYPVKYGEKCTWDTNGPVI PVVYDFGDAQKTASYSPYQREFTAGFVQFRV 240  
 Db 181 HNLFGIYQKYPVKYGEKCTWDTNGPVI PVVYDFGDAQKTASYSPYQREFTAGFVQFRV 240  
 QY 241 FNNEAANALCAGMRVTGCTNHHICGGGVEPEASPOQCGDFSGFDSGYGTHVGYSSS 300  
 Db 241 FNNEAANALCAGMRVTGCTNHHICGGGVEPEASPOQCGDFSGFDSGYGTHVGYSSS 300  
 QY 301 REITEAAVLFFY 312  
 Db 301 REITEAAVLFFY 312

## RESULT 5

ID ITLN2 HUMAN STANDARD; PRT; 325 AA.  
 AC ORNWUT;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DE 13-SEP-2005 (Rel. 48, Last annotation update)  
 GN Intelectin-2 precursor (Endothelial lectin HU-2).  
 GN Name=ITLN2; ORFNames=UNQ2789/PRO7179;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=21096266; PubMed=1181563; DOI=10.1093/glycob/11.1.65;  
 RA Lee J.K., Schnee J., Pang M., Wolfert M., Baum L.G., Moremen K.W.,  
 RT Pierce M.;  
 RL "Human homologs of the Xenopus oocyte cortical granule lectin XL35.";  
 RN Glycobiology 11:65-73(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vects A.,  
 Vanden R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,  
 Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 RA Wood W.I., Godowski P.J., Gray A.M., Zhang Z., Goddard A.D.,  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genomics 13:2265-2270(2003).  
 CC -1- FUNCTION: May play a role in the defense system against pathogens  
 CC (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -1- TISSUE SPECIFICITY: Expressed only in the small intestine.  
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC removed.  
 CC -----  
 CC EMBL: AY065973; AAL58074.1; -; mRNA.  
 DR EMBL: AY358905; AAQ89264.1; -; mRNA.  
 DR Ensembl: ENSG00000158764; Homo sapiens.  
 DR HGNC: HGNC:20599; ITLN2.  
 DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; Fibrinogen\_C; 1\_  
 DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; FALSE\_NEG.  
 KW Lectin; Polymorphism; Signal.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 325 Intelectin-2.  
 FT DOMAIN 45 210 Fibrinogen C-terminal.  
 FT VARIANT 103 103 R -> H (in dbSNP:6680969).  
 FT /FTID=VAR.019926.  
 SQ SEQUENCE 325 AA; 36212 MW; 283C9A1ZAE2DEBFC CRC64;

Query Match 83.0%; Score 1449.5; DB 1; Length 325;  
 Best Local Similarity 83.0%; Pred. No. 1.3e-111;  
 Matches 264; Conservative 18; Mismatches 31; Indels 5; Gaps 3;

QY 1 MNQLSFLFLIATTRGWSMTDEANTYFKETWCSSPSLPRSCKEIKDCPSAFDGL 55  
 Db 8 MTRLCFLFLFSVATSCSAASLSEMLGREPTECAFSSLSLPRSCKEIKERCHSAGDGL 67  
 QY 56 YFLRTENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWSSQQGSKADYPEGD 115  
 Db 68 YFLRTKNGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWSSQQGSKADYPEGD 127  
 QY 116 NWANYNTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPKNSPMQHWNSLLRYRTDTGF 175  
 Db 128 NWANYNTFGSAEAATSDDYKNPGYDIQAKDLGIWHVPKNSPMQHWNSALLRYRTWTF 187  
 QY 176 LQTLGHNLFGIYQKYPVKYGEKCTWDTNGPVI PVVYDFGDAQKTASYSPYQREFTAGP 235  
 Db 188 LQRLGHNLFGIYQKYPVKYRSGKWNNDNGPAIPVYDFGDAKTASYSPYQREFTAGP 247  
 QY 236 VQFRVFNNEAANALCAGMRVTGCTNHHICGGGVEPEASPOQCGDFSGFDSGYGTHV 295  
 Db 248 VQFRVFNNEAANALCAGIKVTGCTNHHICGGGVEPEASPOQCGDFSGFDSGYGTHV 307  
 QY 296 GYSSRSREITEAAVLFFY 313  
 Db 308 KSSCSREITEAAVLFFY 325

RESULT 6  
 OS VY10 HUMAN  
 ID QSVY10 HUMAN PRELIMINARY; PRT; 325 AA.  
 AC QSVY10;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Intelectin 2.  
 GN Name=ITLN2; ORFNames=RP11-312J18.8-001;





PIR; JEO328; JEO328.  
 Ensembl; ENSMUSG00000038209; Mus musculus.  
 MGI; MGI:1333831; Itlna.  
 GO; GO:0005615; C:extracellular space; TAS.  
 GO; GO:0009624; P:response to nematodes; IDA.  
 InterPro; IPR002181; Fibrinogen C.  
 Pfam; PF00147; Fibrinogen\_C\_1.  
 SMART; SM00186; FBG; 1.  
 PROSITE; PS00514; FIBRIN AG C DOMAIN; FALSE NEG.  
 GPI-anchor; Lactin; Lipoprotein; Membrane; Signal.  
 SIGNAL 1 19 By similarity.  
 CHAIN 20 298 Potential.  
 PROPEP 299 313 Intelectin-1a.  
 FT DOMAIN 36 211 Fibrinogen C-terminal.  
 FT LIPID 298 298 GPI-anchor amidated serine (Potential).  
 SQ SEQUENCE 313 AA; 34953 MW; D2FA447D3D8547A4 CRC64;

Query Match 81.7%; Score 1427; DB 1; Length 313;  
 Best Local Similarity 81.5%; Pred. No. 9.3e-110;  
 Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MNQLSFLFLIATTRGWSDEANTYFKWTCSSSPSLPRSCKEIKDPCPSAFDGLYFLRT 60  
 DB 1 MTQLGFLFLIATTRGWSDEANTYFKWTCSSSPSLPRSCKEIKDPCPSAFDGLYFLRT 60  
 QY 61 ENGVIYQTFCDMTSGGGGWTILVASVHENDMRGKCTVGDWRSSQGGKADYPEGDGNWANY 120  
 DB 61 KNGVIYQTFCDMTAGGGWTILVASVHENDMRGKCTVGDWRSSQGGKADYPEGDGNWANY 120  
 QY 121 NTFGSAEAATSDDDYKNPGYDIQADLGIWHVPNKSQMHWRNSSLRLRYRTDTGFLQTLG 180  
 DB 121 NTFGSAEAATSDDDYKNPGYDIQADLGIWHVPNKSQMHWRNSSLRLRYRTDTGFLQTLG 180  
 QY 181 HNLFGIYQKYPVKYGEKCTWDNGVPVIVVYDFGDAQKTASYSPYQOREFTAGVQPRV 240  
 DB 181 HNLFGIYQKYPVKYGEKCTWDNGVPVIVVYDFGDAQKTASYSPYQOREFTAGVQPRV 240  
 QY 241 FNNRAAALCAGVRVTGCTNTEHHCIGGGYFPPEASPOCGDFSGFDMWGYGTHVGYSSS 300  
 DB 241 FNNRAAALCAGVRVTGCTNTEHHCIGGGYFPPEASPOCGDFSGFDMWGYGTHVGYSSS 300  
 QY 301 REITEAAVLLFYR 313  
 DB 301 RKITEAAVLLFYR 313

RESULT 8  
 QSIWS3\_MOUSE PRELIMINARY; PRT; 313 AA.  
 AC QSIWS3;  
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)  
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)  
 DE Intelectin 1.  
 GN Name=Itlna; Synonyms=Itln1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NIH Swiss; TISSUE=Ovary;  
 RA Peavy T.R., Hedrick J.L.;  
 RT "Mouse homolog of the Xenopus laevis egg cortical granule lectin."  
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY619693; AAU8049.1; -; mRNA.  
 DR MGI; MGI:1333831; Itlna.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0009624; P:response to nematodes; IDA.  
 SQ SEQUENCE 313 AA; 34953 MW; D2FA447D3D8547A4 CRC64;

Query Match 81.7%; Score 1427; DB 2; Length 313;  
 Best Local Similarity 81.5%; Pred. No. 9.3e-110;  
 Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MNQLSFLFLIATTRGWSDEANTYFKWTCSSSPSLPRSCKEIKDPCPSAFDGLYFLRT 60  
 DB 1 MTQLGFLFLIATTRGWSDEANTYFKWTCSSSPSLPRSCKEIKDPCPSAFDGLYFLRT 60  
 QY 61 ENGVIYQTFCDMTSGGGGWTILVASVHENDMRGKCTVGDWRSSQGGKADYPEGDGNWANY 120  
 DB 61 KNGVIYQTFCDMTAGGGWTILVASVHENDMRGKCTVGDWRSSQGGKADYPEGDGNWANY 120  
 QY 121 NTFGSAEAATSDDDYKNPGYDIQADLGIWHVPNKSQMHWRNSSLRLRYRTDTGFLQTLG 180  
 DB 121 NTFGSAEAATSDDDYKNPGYDIQADLGIWHVPNKSQMHWRNSSLRLRYRTDTGFLQTLG 180  
 QY 181 HNLFGIYQKYPVKYGEKCTWDNGVPVIVVYDFGDAQKTASYSPYQOREFTAGVQPRV 240  
 DB 181 HNLFGIYQKYPVKYGEKCTWDNGVPVIVVYDFGDAQKTASYSPYQOREFTAGVQPRV 240  
 QY 241 FNNRAAALCAGVRVTGCTNTEHHCIGGGYFPPEASPOCGDFSGFDMWGYGTHVGYSSS 300  
 DB 241 FNNRAAALCAGVRVTGCTNTEHHCIGGGYFPPEASPOCGDFSGFDMWGYGTHVGYSSS 300  
 QY 301 REITEAAVLLFYR 313  
 DB 301 RKITEAAVLLFYR 313

RESULT 9  
 ITL1B\_MOUSE STANDARD; PRT; 313 AA.  
 AC Q80ZA0;  
 DT 01-FEB-2005 (Rel. 46, Created)  
 DT 01-FEB-2005 (Rel. 46, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Intelectin-1b precursor (Intelectin-2).  
 GN Name=Itlnb; Synonyms=Itln2, Itlnb;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/c; TISSUE=Intestine;  
 RA PubMed=15265922; DOI=173/3/1894;  
 RA Pemberton A.D., Knight P.A., Gamble J., Colledge W.H., Lee J.K.,  
 RA Pierce M., Miller H.R.;  
 RT "Innate BALB/c enteric epithelial responses to Trichinella spiralis:  
 RT inducible expression of a novel goblet cell lectin, intelectin-2, and  
 RT its natural deletion in C57BL/10 mice."  
 RL J. Immunol. 173:1894-1901(2004).  
 CC -!- FUNCTION: May play a protective role in the innate immune response  
 CC to parasite infection.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC Also secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Expressed in the goblet and Paneth cell of  
 CC small intestine of infected mice. Expressed in the ileum of  
 CC uninfected mice.  
 CC -!- INDUCTION: Up-regulated early (day 3) during infection with  
 CC parasite and level remained high through to day 14, time of  
 CC parasite rejection.  
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
 CC -!- CAUTION: The two mouse genes Itlna and Itlnb are the paralogs of  
 CC human ITLN1.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AY217760; AAO60215.1; -; mRNA.



SQ SEQUENCE 338 AA; 37560 MW; 2FF842F74797A81D CRC64;  
 Query Match 63.3%; Score 1105.5; DB 2; Length 338;  
 Best Local Similarity 63.3%; Pred. No. 4.1e-83;  
 Matches 197; Conservative 40; Mismatches 65; Indels 9; Gaps 2;  
 QY 7 LLFLIATTCGWSDEANTYKFWTCS-----SSSLPRSKKEIKDECPSPAFDGLYFLRTEN 62  
 DB 33 ILGLASWEDYSCSKNGF-----CSHNKSKSKMYRNCRKEIKFNNAEDGIYTLRTGG 87  
 QY 63 GVITYQTCMDTSGGGTLLVASVHENDMRGKCTVGDWSSQGSKADYPEGDGNWANT 122  
 DB 88 GISYQTCMDTADGGTLLVASVHENNMFCKTVDGRTWSQGNPDNTPAGDGNWANT 147  
 QY 123 FGSAAEATSDYKPCGYDIOAKDLGIHVVPKNSPQWHRNSSLRYRTDTGFLQTLGHN 182  
 DB 148 FGLPGGATSDYKPCGYDITSNGLMWHVPNNTPFWSHRNSSLRYRTQNNFSAEGN 207  
 QY 183 LFGIYQYKPVKYGEGKCTWTDNGVPVVDGDAQKTSYSPYQOREFTAGFVQFRVFN 242  
 DB 208 LFNLYQYKPLKFGIGTCPCDHPGPAVPIYDIGNPDLTKYSPSGRREFTAGFVHFRVFN 267  
 QY 243 NERAANALCAGMRVTGNTGHEHCIGGGYFFPASPQCGDFSGDWSGTHVGYSSRE 302  
 DB 268 AKAAALCAGVVKVVGNTGHEHCIGGGYFAEGNPKQCGDFTGPDWDGTYGTHQDWSNKE 327  
 QY 303 ITEAAVLLFYR 313  
 DB 328 ITEAAVLLFYR 338  
 RESULT 12  
 ID Q800K0\_XENLA PRELIMINARY; PRT; 342 AA.  
 AC Q800K0;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Embryonic epidermal lectin.  
 GN Name=XEEL;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22739598; PubMed=12802587; DOI=10.1007/s00427-003-0341-9;  
 RA Nagata S., Nakanishi M., Namba R., Fujita N.;  
 RT "Developmental expression of XEEL, a novel molecule of the Xenopus  
 oocyte cortical granule lectin family.";  
 RL Dev. Genes Evol. 213:368-370(2003).  
 DR EMBL; AB105372; BAC65329.1; -; mRNA.  
 DR GO; GO:0005249; F: sugar binding; IEA.  
 DR GO; GO:0007596; P: blood coagulation; IEA.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; Fibrinogen\_C.  
 DR SMART; SM00186; FBG; 1.  
 KW Lectin.  
 SQ SEQUENCE 342 AA; 37294 MW; 9FCD955184B168B6 CRC64;  
 Query Match 63.1%; Score 1103; DB 2; Length 342;  
 Best Local Similarity 61.7%; Pred. No. 6.7e-83;  
 Matches 209; Conservative 32; Mismatches 72; Indels 26; Gaps 4;  
 QY 1 MNQLSFLFLIATTCG--WSTDEANTYFKE-----WT-----CSSSPSLP--- 38  
 DB 4 MLSYLLLPALFPAGHAGSCQASISEKKEIKLLNLLACWTEGNADNSLSRSGSPGDM 63  
 QY 39 -----PSCKEIKDECPSPAFDGLYFLRTENGVIYQFCDMTSGGGTLLVASVHENDMRGKC 94  
 DB 64 NYGYSRSCNEIKSSDSRAPDGIYTLATDGEISYQFCDMTNGGGTLLVASVHENDMRGKC 123  
 QY 95 TVGDRWSSQGSKADYPEGDGNWANTFGSAAEATSDYKPCGYDIOAKDLGIHVVPN 154  
 DB 124 TVGDRWSTQGNLQNPGEQGNWANTFGLPEGATSDYKPCGYDIEAKNLALMHPVN 183  
 QY 155 KSPMQWHRNSSLRYRTDTGFLQTLGHNLFYIYQYKPVKYGEGKCTWTDNGVPVVDG 214  
 DB 184 KTPMVWHRNSSLRYRTQNTGFLTEGGNLFELYKPYKYGEGKCTWTDNGVPVVDG 243  
 QY 215 DAQKTASYSPYQOREFTAGFVQFRVFNERRAANALCAGMRVTGNTGHEHCIGGGY 274  
 DB 244 SAEKTASLYSPNGRSEFTAGFVQFRVFNTERATLALCAGVVKVGCNVEHCIGGGY 303  
 QY 275 ASPQCGDFSGDWSGTHVGYSSREITEAAVLLFYR 313  
 DB 304 ASPQCGDFSGDWSGTHVGYSSREITEAAVLLFYR 342  
 RESULT 13  
 ID Q5PPM0\_XENLA PRELIMINARY; PRT; 339 AA.  
 AC Q5PPM0;  
 DT 01-FEB-2005 (TRENBLrel. 29, Created)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
 DE XEEL protein.  
 GN Name=XEEL;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
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 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
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 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
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 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 Scherch A

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Query Match 62.7%; Score 1095; DB 2; Length 339;
Best Local Similarity 60.9%; Pred. No. 3e-82;
Matches 206; Conservative 34; Mismatches 70; Indels 28; Gaps 4;

QY 4 LSPFLFIATY-----RGWSTDEANTYFKB-----WT-----CSSSPSLP----- 38
DB 2 LSYSLLLALLAFAPAGHAGSCQASISBKEKILNLLACWTEGNADNLSRSGSPGDMN 61

QY 39 ---RSCKEIKDCPSAFDGLYRTENGVIYQFCDMTSGGGWTLVASVHENDMRGKCT 95
DB 62 YGRSCNEIKSSDSRAPDGLYRTATEDGESYQFCDMITNGGGWTLVASVHENDMRGKCT 121

QY 96 VGRDWSQQSKADYPEGDGNWANTYTFGSAEATSDDYKNPGYDIOAKDLGIWVFNPK 155
DB 122 VGRDWSQQGNLQNPEDGDNWANYATFGLPEGATSDDYKNPGYDIEAKNLALMHVFNPK 181

QY 156 SPQHWNRNSSLRYRTDTGFLQTLGNLFGIYQKYPVKYGEKWTNDGVPVIVVYDPGD 215
DB 182 TPMVMNRNSSLRYRTQNGFLTEGGNLFELYKYPVKYDIGNKLDNGPAPVIVVYDLGS 241

QY 216 AOKTASVSPYQREFTAGVQVRFVFNNEAANALCAGMRVTGNTTEHHCIGGGYFPEA 275
DB 242 AETASLYSPNGSEFTPGVQVFRANSEKATLALCAGVKVKGCVNVEHHCIGGGYIPEG 301

QY 276 SPQCGDFSGDFMGYGVTHVGYSSREITEAAVLLFYR 313
DB 302 SPQCGDFPAAALWDGVTNLGWSASKQIIEAAVLLFYR 339

RESULT 14
Q8JJC9 XENLA
ID Q8JJC9 XENLA PRELIMINARY; PRT; 315 AA.
AC Q8JJC9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Lectin type 2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Iehino T., Sekimizu K., Natori S., Kubo T.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB061239; BAB91360.1; -; mRNA.
DR GO; GO:0007596; P: blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C.
DR SMART; SM00186; FBG; 1.
SQ SEQUENCE 315 AA; 34329 MW; 515C3G5F7F12B69A CRC64;

Query Match 61.8%; Score 1080; DB 2; Length 315;
Best Local Similarity 63.7%; Pred. No. 4.8e-81;
Matches 198; Conservative 33; Mismatches 78; Indels 2; Gaps 1;

QY 5 SPFLFIATRGWSTDEANTYFKWT-----CSSPSLPRSCKEIKDCPSAFDGLYFLRTEN 62
DB 5 SLLLVLLI1TGTCTRTFPFSLHPEYPTGTTSESSNGFNRCKEIKDSDSAKOGIYNLITAN 64

QY 63 GVITYQFCDMTSGGGWTLVASVHENDMRGKCTVGRDWSQQSKADYPEGDGNWANYT 122
DB 65 GETYQAFCDMTDGGGWTLVASVHENDMRGKCTVGRDWSQQGNNTNPFGEENWANYAT 124

QY 123 FGSAAEATSDDYKNPGYDIOAKDLGIWVFNPKSPQHWNRNSSLRYRTDTGFLQTLGN 182
DB 125 FGLPEGATGDDYKNPGYDIISAKDLAIWVFNPNTPMTWSRSSLRYRTSNGFPFSEGN 184

QY 183 LFGIYQKYPVKYGEKWTNDGVPVIVVYDFGDAKTASVSPYQREFTAGVQVRFVN 242
DB 185 LFNLYKYPVIVNTGSCQTNNGPAPVLYDFGDPKTTSMYSPNGRGEFTAGVQVRFVN 244
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QY 243 NERAANALCAGMRVTGNTTEHHCIGGGYFPBRASPOCGDFSGDFMGYGVTHVGYSSRE 302
DB 245 TERAPALCPGKIVTGCNAEHHHCIGGGFIPGPNVQCGDFAAFDWNNGYGTGYAMSSITKA 304

QY 303 ITEAAVLLFYR 313
DB 305 ITEAAVLLMYR 315

RESULT 15
Q91719 XENLA
ID Q91719 XENLA PRELIMINARY; PRT; 313 AA.
AC Q91719;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cortical granule lectin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Chang B.Y., Wardrip N.J., Hedrick J.L.;
RL Molecular cloning and characterization of cortical granule lectin: an essential glycoprotein involved in the block of polyspermy.
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DE Lectin.
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Hedrick J.L.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; X82626; CAA57946.1; -; mRNA.
DR PIR; S49589; S49589.
DR GO; GO:0005529; F: sugar binding; IEA.
DR GO; GO:0007596; P: blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR SMART; SM00186; FBG; 1.
KW Lectin.
FT CHAIN 16 313 Potential.
SQ SEQUENCE 313 AA; 34304 MW; 519762656B82507E CRC64;

Query Match 60.1%; Score 1049.5; DB 2; Length 313;
Best Local Similarity 61.5%; Pred. No. 1.6e-78;
Matches 192; Conservative 37; Mismatches 72; Indels 11; Gaps 2;

QY 8 LFLIATRGWSTD-----EANTYFKWTCSPPSLPRSCKEIKDCPSAFDGLYFLRT 60
DB 5 IILLVLTGLSQCSPVIVASKNVWKQLDCKP-----RSCKEIKDSDNEAQDITLTS 60

QY 61 ENGVIYQFCDMTSGGGWTLVASVHENDMRGKCTVGRDWSQQSKADYPEGDGNWANY 120
DB 61 SDGISVQTECDMTTNGGGWTLVASVHENDMRGKCTVGRDWSQQGNRADYPEGDGNWANY 120

QY 121 NTFGSABAATSDDYKNPGYDIOAKDLGIWVFNPKSPQHWNRNSSLRYRTDTGFLQTLG 180
DB 121 NTFGSAGGATSDDYKNPGYDIEAYNLGVMHVPNKTPLSVNRNSSLRYRTDTGILFKHG 180

QY 181 HNLFGIYQKYPVKYGEKWTNDGVPVIVVYDFGDAKTASVSPYQREFTAGVQVRFVN 240
DB 181 GNLFSLRYIYVYKYGKSCDSGTPVIVVYDLGSAKLTAISYSPDPSQFTPGYIQFRP 240

QY 241 FNNERAANALCAGMRVTGNTTEHHCIGGGYFPEASPOCGDFSGDFMGYGVTHVGYSSS 300
DB 241 INTERAALALCFGMKMSCNVEHVCIGGGYFPEADPRCGDFAAFDNGYGTGKFNESAG 300

QY 301 REITRAAVLLFY 312
DB 301 IBITRAAVLLFY 312
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Thu Feb 9 11:59:17 2006

us-10-063-595-88.multi.rup

Page 20

Search completed: February 8, 2006, 19:42:23  
Job time : 307 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 8, 2006, 19:37:48 ; Search time 43 Seconds  
(without alignments)  
700.369 Million cell updates/sec

Title: US-10-063-595-88

Perfect score: 1747

Sequence: 1 MNQLSFLPLIATIRGWSTD.....HVGYSRSREITEAAVLLPYR 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1427	81.7	313	2 JE0328	intelectin - mouse
2	866.5	49.6	302	2 S49589	cortical granule 1
3	129.5	7.4	282	2 A35084	fibrinogen-related
4	109	6.2	491	1 FGHUB	fibrinogen beta ch
5	107.5	6.2	1045	2 S23570	pol polyprotein ho
6	105.5	6.0	189	2 C81428	peptidyl-prolyl ci
7	105.5	6.0	616	2 T32131	hypothetical prote
8	100	5.7	2265	1 FNBO	fibronectin - bovi
9	99	5.7	328	2 A05299	fibrinogen beta ch
10	99	5.7	444	2 S05313	fibrinogen gamma-B
11	99	5.7	796	1 JV0107	glucose dehydrogen
12	99	5.7	796	2 H85495	glucose dehydrogen
13	99	5.7	796	2 H90644	glucose dehydrogen
14	98.5	5.6	725	2 H81030	TonB-dependent rec
15	97	5.6	496	1 A46725	omega-crystallin -
16	95.5	5.5	450	2 S38114	hypothetical prote
17	95.5	5.5	463	2 A38463	fibrinogen beta ch
18	95.5	5.5	479	2 A25052	fibrinogen beta ch
19	95	5.4	725	2 D81976	probable ferric ai
20	94.5	5.4	649	2 D90496	hypothetical prote
21	94	5.4	1018	2 AG2556	hypothetical prote
22	93.5	5.4	551	1 A31389	beta-amyase (EC 3
23	93	5.3	468	1 FGBOB	fibrinogen beta ch
24	92.5	5.3	1332	2 T23024	hypothetical prote
25	92	5.3	796	2 AG0523	glucose dehydrogen
26	91	5.2	493	2 JC3027	type 1 angiotensin
27	90	5.2	2201	2 A32160	tenascin-C - human
28	89.5	5.1	600	2 I49281	fertilin alpha pre
29	89.5	5.1	1054	2 T18304	acid trehalase hom

tenascin precursor  
ficolin-1 precursor  
homeotic protein p  
hypothetical prote  
hypothetical prote  
NCA3 protein precu  
alpha-amyase (EC  
pullulanase - spin  
tenascin Y precurs  
hypothetical prote  
hypothetical prote  
uncharacterized pr  
glutamate-ammonia  
lysine 6-monooxyge  
alpha-glucosidase  
hypothetical prote  
ficolin-A precursor  
starch synthase (E  
notch protein homo  
hemagglutinin prec  
janusin precursor,  
fibrinogen alpha c  
collagen alpha 1(X  
collagen alpha 1(V  
hypothetical prote  
alpha-xylosidase -  
nebulin, skeletal  
chitinase (EC 3.2.  
genome polyprotein  
pectate lyase (EC  
pectate lyase (EC  
hypothetical prote  
glucan 1,4-alpha-m  
hypothetical prote  
nitrogenase (EC 1.  
NADH2 dehydrogenas  
proteins F1E22.10 l  
hypothetical prote  
histone deacetylase  
HE65 protein - Aut  
probable RNA-direc  
tenascin precursor  
fibronectin precur  
fibronectin-related  
histone deacetylase  
F2023.27 protein  
probable chitinase  
hypothetical prote  
TonB-dependent rec  
type 4 fibrinial bi  
structural polypro  
tenascin-X - bovin  
tenascin homolog -  
outer membrane por  
outer membrane por  
glutamate-ammonia  
tenascin-X - pig (c  
cellulase (EC 3.2.  
metalloproteinase  
pyruvate decarboxy  
probable succinate  
serine/threonine-p  
cysteine proteinase  
hypothetical prote  
starch synthase (E  
cytotactin - chick  
genome polyprotein  
alpha-amyase (EC  
alkaline serine pr  
hypothetical prote  
fibronectin precur  
intrinsic factor-B

103	81	4.6	378	2	S36506	E2 protein - human	176	78.5	4.5	2481	2	A43908	fibronectin - Afri
104	81	4.6	432	2	A27447	cytotoxic T-lympho	177	78	4.5	349	2	T06207	cysteine proteinas
105	81	4.6	528	2	G02127	fus-like protein -	178	78	4.5	397	2	E86304	F611.9 protein - A
106	81	4.6	603	2	T48154	pyruvate decarboxy	179	78	4.5	404	2	B84745	probable RNA-bind
107	81	4.6	641	1	A41932	fibrinogen alpha-I	180	78	4.5	584	2	T06163	beta-fructofuran
108	81	4.6	792	2	B82756	organic solvent to	181	78	4.5	611	2	S60040	alpha-amylase (EC
109	81	4.6	817	2	S77106	hypothetical prote	182	78	4.5	706	2	T12748	NADH2 dehydrogen
110	81	4.6	872	2	H75564	probable ATP-depen	183	78	4.5	795	2	T43447	hypothetical prote
111	81	4.6	890	2	T35237	probable secreted	184	78	4.5	813	2	A40601	hypothetical prote
112	81	4.6	940	2	AD1374	internalin protein	185	78	4.5	815	2	H83345	ferripyoverdine re
113	81	4.6	1028	2	T03516	probable outer mem	186	78	4.5	986	2	T49914	thermoactive cellu
114	81	4.6	2403	2	A59386	sanko - human	187	78	4.5	1963	2	T49914	callose synthase c
115	80.5	4.6	319	2	T40156	sun family protein	188	77.5	4.4	189	1	CUWOI	insecticynanin B -
116	80.5	4.6	334	2	T20524	hypothetical prote	189	77.5	4.4	206	2	S22401	probable beta-gluc
117	80.5	4.6	375	2	T33757	hypothetical prote	190	77.5	4.4	577	2	T02401	transport protein
118	80.5	4.6	548	1	HYBSS	bacillolysin (EC 3	191	77.5	4.4	586	2	T52148	probable flavoprot
119	80.5	4.6	841	2	E71808	probable iron (III	192	77.5	4.4	597	2	S76209	threonyl-trNA synt
120	80.5	4.6	867	1	C64785	outer membrane uah	193	77.5	4.4	635	2	D82770	succinate dehydrog
121	80.5	4.6	869	2	B85553	hypothetical prote	194	77.5	4.4	640	2	S34793	glucan 1,4-alpha-m
122	80.5	4.6	869	2	B90703	pyruvate decarboxy	195	77.5	4.4	677	2	JC7202	glutenin high mole
123	80.5	4.6	3566	1	A40701	tenascin-X precurs	196	77.5	4.4	830	2	S15720	iron(III) dicitrat
124	80.5	4.6	4199	2	S76412	hypothetical prote	197	77.5	4.4	842	2	H64694	complement factor
125	80	4.6	297	2	D69866	hypothetical prote	198	77.5	4.4	1234	1	NEMSH	ice nucleation pro
126	80	4.6	405	2	S65471	hypothetical prote	199	77.5	4.4	1258	2	JQ0188	insulin receptor-r
127	80	4.6	432	2	I56934	pyruvate decarboxy	200	77.5	4.4	1268	2	B36502	hypothetical prote
128	80	4.6	439	2	I37391	fibrinogen-like pr	201	77.5	4.4	3016	2	S77300	endo-1,4-beta-xyla
129	80	4.6	815	2	B30843	fibrinogen-like pr	202	77	4.4	240	1	J80591	hypothetical prote
130	80	4.6	946	2	G71617	glutenin high mole	203	77	4.4	274	2	T31528	hypothetical prote
131	80	4.6	1519	2	S41525	SERA antigen/papal	204	77	4.4	286	2	D83762	transcription regu
132	80	4.6	1746	1	S18694	major ring-forming	205	77	4.4	390	2	R44086	hypothetical prote
133	79.5	4.6	323	2	A47172	tenascin precursor	206	77	4.4	392	2	T25213	hypothetical prote
134	79.5	4.6	372	2	A42778	transforming growt	207	77	4.4	418	2	AF2045	sugar transport sy
135	79.5	4.6	385	2	T26404	agglutinin precurs	208	77	4.4	437	1	FGHUG	fibrinogen gamma-A
136	79.5	4.6	626	2	T01485	hypothetical prote	209	77	4.4	453	1	FGHUGB	fibrinogen gamma-B
137	79.5	4.6	750	2	T10864	probable polygalac	210	77	4.4	459	2	A25928	endo-beta-1,4-gluc
138	79.5	4.6	750	2	B87636	transcription acti	211	77	4.4	460	2	JC1299	hypothetical prote
139	79.5	4.6	970	2	I78842	receptor protein-t	212	77	4.4	461	2	T20163	endoglucanase I -
140	79.5	4.6	986	2	T03760	TonB-dependent rec	213	77	4.4	464	2	JC7143	hypothetical prote
141	79.5	4.6	1196	2	A29130	pullulanase (EC 3	214	77	4.4	551	2	B64005	hemagglutinin prec
142	79.5	4.6	2236	1	Q2FP	beta-amylase (EC 3	215	77	4.4	564	1	HMIVF5	vitamin B12 recept
143	79.5	4.6	2489	2	T29285	rudimentary protei	216	77	4.4	614	2	AB0935	thrombin (EC 3.4.2
144	79.5	4.6	2761	1	PGRTGA	complement C3b/C4b	217	77	4.4	618	2	A35827	coagulation factor
145	79	4.5	437	1	PGRTGA	fibrinogen gamma-A	218	77	4.4	668	2	A46013	agrobacterium viru
146	79	4.5	445	1	FGRTGB	fibrinogen gamma-B	219	77	4.4	737	2	AI3179	tenascin-X - mouse
147	79	4.5	448	2	C98122	choline binding pr	220	77	4.4	860	2	I48839	probable outer mem
148	79	4.5	544	2	S76859	hypothetical prote	221	77	4.4	866	1	C64834	phosphoribosylform
149	79	4.5	649	2	AH3546	outer membrane pro	222	77	4.4	1358	2	S64356	probable tenascin
150	79	4.5	919	2	S33942	hexon protein - hu	223	77	4.4	4006	2	T09070	conserved hypothet
151	79	4.5	928	2	T20035	hypothetical prote	224	76.5	4.4	154	2	B69840	endo-1,4-beta-xyla
152	79	4.5	971	2	H71719	hypothetical prote	225	76.5	4.4	241	2	T37005	vestigial protein
153	78.5	4.5	300	2	E71534	probable pbp2b met	226	76.5	4.4	433	2	A46440	acid phosphatase (
154	78.5	4.5	302	2	D81692	conserved hypothet	227	76.5	4.4	464	1	B59200	aldehyde dehydrog
155	78.5	4.5	412	2	C84518	hypothetical prote	228	76.5	4.4	479	2	B87301	beta-xylosidase, f
156	78.5	4.5	482	2	B31795	collagen alpha 1(X	229	76.5	4.4	533	2	C97324	hypothetical prote
157	78.5	4.5	535	2	T32139	hypothetical prote	230	76.5	4.4	541	2	D83684	hypothetical prote
158	78.5	4.5	698	2	T01209	starch synthase (E	231	76.5	4.4	699	2	A38368	conserved hypothet
159	78.5	4.5	698	2	F64839	yegH protein precu	232	76.5	4.4	706	2	AD0173	polypeptide - hepa
160	78.5	4.5	764	2	H83055	probable outer mem	233	76.5	4.4	716	2	JQ1366	complement factor
161	78.5	4.5	770	2	S76095	hypothetical prote	234	76.5	4.4	763	2	I50807	hypothetical prote
162	78.5	4.5	781	2	T35029	hypothetical prote	235	76.5	4.4	941	2	T32449	ice nucleation pro
163	78.5	4.5	837	2	H87638	TonB-dependent rec	236	76.5	4.4	1322	2	S07053	mannose receptor p
164	78.5	4.5	900	2	T19689	hypothetical prote	237	76.5	4.4	1456	1	A36563	hypothetical prote
165	78.5	4.5	914	2	C92884	surface layer prot	238	76.5	4.4	2129	2	T16199	C-5 cytosine-speci
166	78.5	4.5	1002	2	B81180	probable oxidoredu	239	76	4.4	337	2	A81101	transcription regu
167	78.5	4.5	1002	2	C60266	probable oxidoredu	240	76	4.4	433	1	S22284	choline binding pr
168	78.5	4.5	1005	2	C71513	hypothetical prote	241	76	4.4	448	2	C95257	hypothetical prote
169	78.5	4.5	1139	1	E64234	cytadherence-aceg	242	76	4.4	452	2	T26827	endo-1,4-beta-gluc
170	78.5	4.5	1249	2	S68431	tripeptidyl-peptid	243	76	4.4	460	2	I40799	metalloproteinase
171	78.5	4.5	1262	2	I48855	tripeptidyl-peptid	244	76	4.4	475	2	S48132	nitrogenase (EC 1.
172	78.5	4.5	1431	2	A45866	dextranucrase (EC	245	76	4.4	515	1	NI2JAM	hemagglutinin prec
173	78.5	4.5	1436	2	A46496	collagen alpha 1(V	246	76	4.4	564	1	HMIVP2	hypothetical prote
174	78.5	4.5	1838	1	CGHU1V	complement recepto	247	76	4.4	565	2	T16318	catechol oxidase (
175	78.5	4.5	2014	2	I36936		248	76	4.4	583	2	S34785	

fibronectin - Afri  
cysteine proteinas  
F611.9 protein - A  
probable RNA-bind  
beta-fructofuran  
alpha-amylase (EC  
NADH2 dehydrogen  
hypothetical prote  
ferripyoverdine re  
thermoactive cellu  
callose synthase c  
insecticynanin B -  
probable beta-gluc  
transport protein  
probable flavoprot  
threonyl-trNA synt  
succinate dehydrog  
glucan 1,4-alpha-m  
glutenin high mole  
iron(III) dicitrat  
complement factor  
ice nucleation pro  
insulin receptor-r  
hypothetical prote  
endo-1,4-beta-xyla  
hypothetical prote  
transcription regu  
hypothetical prote  
hypothetical prote  
sugar transport sy  
fibrinogen gamma-A  
fibrinogen gamma-B  
cellulase (EC 3.2.  
endo-beta-1,4-gluc  
hypothetical prote  
endoglucanase I -  
hemagglutinin prec  
vitamin B12 recept  
thrombin (EC 3.4.2  
coagulation factor  
agrobacterium viru  
tenascin-X - mouse  
probable outer mem  
phosphoribosylform  
probable tenascin  
conserved hypothet  
endo-1,4-beta-xyla  
vestigial protein  
acid phosphatase (  
aldehyde dehydrog  
beta-xylosidase, f  
hypothetical prote  
conserved hypothet  
chitinase (EC 3.2.  
polypeptide - hepa  
complement factor  
hypothetical prote  
ice nucleation pro  
mannose receptor p  
hypothetical prote  
C-5 cytosine-speci  
transcription regu  
choline binding pr  
hypothetical prote  
endo-1,4-beta-gluc  
metalloproteinase  
nitrogenase (EC 1.  
hemagglutinin prec  
hypothetical prote  
catechol oxidase (



249	76	4.4	522	2	T48155	pyruvate decarboxy	322	74.5	4.3	1353	1	JH0675	restrictin precurs
250	76	4.4	642	1	S34416	transcription fact	323	74.5	4.3	2425	2	D69426	surface layer prot
251	76	4.4	660	2	S70904	transferrin-bindin	324	74.5	4.3	2871	2	A55624	fibrillin-1 precur
252	76	4.4	747	2	H82943	hypothetical prote	325	74	4.2	187	2	S20044	opacity protein op
253	76	4.4	828	2	S52393	beta-galactosidase	326	74	4.2	240	1	S47512	endo-1,4-beta-xyla
254	76	4.4	872	2	S49538	CocC protein precu	327	74	4.2	241	2	S71473	endo-1,4-beta-xyla
255	76	4.4	1608	2	A28182	hemolysin A - Serr	328	74	4.2	280	2	AC1502	hypothetical prote
256	75.5	4.3	324	2	S20981	chitinase (EC 3.2.	329	74	4.2	316	2	F89791	peptidoglycan hydr
257	75.5	4.3	445	2	T44482	lysine 6-monooxyge	330	74	4.2	341	2	T07145	epoxide hydrolase
258	75.5	4.3	473	2	A48949	beta-glucosidase,	331	74	4.2	350	2	B43670	sulfate-binding pr
259	75.5	4.3	484	2	E84765	hypothetical prote	332	74	4.2	365	2	A26459	helix-destabilizin
260	75.5	4.3	530	2	D70480	acetyl-coenzyme A	333	74	4.2	380	2	E88421	protein R74.2 [imp
261	75.5	4.3	536	2	A34901	lysine carboxypept	334	74	4.2	437	2	JC7138	alpha-amylose (EC
262	75.5	4.3	641	2	AI2524	hypothetical prote	335	74	4.2	437	2	TJ0946	alpha-amylose 3E -
263	75.5	4.3	657	2	E81119	tail fibre protein	336	74	4.2	455	2	E96817	hypothetical prote
264	75.5	4.3	703	2	T13074	NADH2 dehydrogenas	337	74	4.2	489	2	C97070	probable aldehyde
265	75.5	4.3	705	1	CIHURB	complement subcomp	338	74	4.2	503	2	C97262	N-terminal domain
266	75.5	4.3	708	2	AH2626	ferrichrome iron r	339	74	4.2	536	2	T51771	poly(3-hydroxybuty
267	75.5	4.3	736	2	T19366	hypothetical prote	340	74	4.2	548	2	AF1231	alpha, alpha-phosph
268	75.5	4.3	747	2	G97408	FeGa protein U6140	341	74	4.2	549	2	T20720	hypothetical prote
269	75.5	4.3	784	2	AI0513	organic solvent to	342	74	4.2	557	2	D97210	extracellular neut
270	75.5	4.3	867	2	D82940	conserved hypothet	343	74	4.2	589	2	T23881	hypothetical prote
271	75.5	4.3	881	2	T31818	hypothetical prote	344	74	4.2	596	1	S33540	catechol oxidase (
272	75.5	4.3	1026	1	TLBP74	tail fiber protein	345	74	4.2	596	2	AI1865	hypothetical prote
273	75.5	4.3	1647	2	T32934	hypothetical prote	346	74	4.2	616	1	A40457	replication protei
274	75.5	4.3	2338	2	T25810	hypothetical prote	347	74	4.2	669	2	T05212	hypothetical prote
275	75.5	4.3	2437	2	S53611	hypothetical prote	348	74	4.2	827	2	AC2963	celB protein [imp
276	75.5	4.3	3411	1	GNWVY	MIBpi protein - ra	349	74	4.2	829	2	T13494	hypothetical prote
277	75.5	4.3	3411	1	GNWVY	genome polypotein	350	74	4.2	837	2	H84239	dimethylsulfoxide
278	75	4.3	238	2	T52505	genome polypotein	351	74	4.2	881	2	B98320	cellulose synthase
279	75	4.3	324	2	AB0767	hypothetical prote	352	74	4.2	975	2	A86258	protein F5011.4 [i
280	75	4.3	329	2	S34493	probable reductase	353	74	4.2	1404	2	E90658	RhsG core protein
281	75	4.3	330	1	S15303	1-phosphatidylinos	354	74	4.2	1466	2	T17138	CL18A protein - ra
282	75	4.3	345	2	E69574	probable CDP-6-deo	355	74	4.2	1467	2	T18411	latrophilin-1, bra
283	75	4.3	358	2	D70797	pectate lyase pels	356	74	4.2	1471	2	T17149	CL18A protein - ra
284	75	4.3	376	2	D87451	probable DNA ligas	357	74	4.2	1503	2	T18266	cycloimulo-oligos
285	75	4.3	376	2	S49886	oxidoreductase, GF	358	74	4.2	1510	2	T17145	CL18B protein - ra
286	75	4.3	551	2	T16557	hypothetical prote	359	74	4.2	1515	2	T17156	CL18B protein - ra
287	75	4.3	584	2	T18908	hypothetical prote	360	74	4.2	1515	2	T17156	genome polypotein
288	75	4.3	586	1	VEHULB	lamin B1 - human	361	74	4.2	3010	1	GNWVY	peroxidase (EC 1.1
289	75	4.3	587	2	S07720	lamin B - mouse	362	73.5	4.2	325	2	S32768	hypothetical prote
290	75	4.3	617	2	S62003	probable ATP-depen	363	73.5	4.2	356	2	T21681	hypothetical prote
291	75	4.3	623	1	S33167	gene pointed prote	364	73.5	4.2	368	2	S47312	cysteine proteinas
292	75	4.3	711	2	S70660	transferrin-bindin	365	73.5	4.2	483	2	H72640	hypothetical prote
293	75	4.3	714	2	T00942	hypothetical prote	366	73.5	4.2	512	2	T23035	hypothetical prote
294	75	4.3	717	1	S28784	alpha-amylose (EC	367	73.5	4.2	574	2	C82301	endoglucanase-rela
295	75	4.3	718	1	S33168	gene pointed prote	368	73.5	4.2	583	1	JC2545	acid phosphatase (
296	75	4.3	760	1	C2MS	classical-compleme	369	73.5	4.2	590	2	A41335	microbial metallo
297	75	4.3	818	2	F87327	conserved hypothet	370	73.5	4.2	618	2	H70552	probable PPE prote
298	75	4.3	1083	2	H86921	probable arabinosy	371	73.5	4.2	774	1	JQ0550	1,4-alpha-glucan b
299	75	4.3	1191	2	AF2501	WD-repeat protein,	372	73.5	4.2	834	2	S66498	M-sema F protein p
300	75	4.3	1240	1	VHWVEV	structural polyp	373	73.5	4.2	908	2	JN0819	transferrin-bindin
301	75	4.3	1241	2	S26373	genome polypotein	374	73.5	4.2	1016	2	T41720	hypothetical prote
302	75	4.3	1242	2	A56605	structural polyp	375	73.5	4.2	1018	1	S73720	cytadherence acces
303	75	4.3	1242	2	S72350	structural polyp	376	73.5	4.2	1166	1	E65151	hypothetical 126K
304	75	4.3	1341	2	S09579	tail fiber protein	377	73.5	4.2	1322	2	D82685	phosphoribosylform
305	75	4.3	1404	2	E85509	hypothetical prote	378	73.5	4.2	2183	1	S37218	hypothetical prote
306	74.5	4.3	326	2	B47172	ficolin-beta - pig	379	73.5	4.2	3011	1	S40770	genome polypotein
307	74.5	4.3	330	2	T34972	probable membrane	380	73.5	4.2	4307	2	T20721	hypothetical prote
308	74.5	4.3	334	2	JB0231	metalloendopeptida	381	73	4.2	99	2	F82467	hypothetical prote
309	74.5	4.3	335	2	T03230	membrane protein,	382	73	4.2	165	2	A28351	probable plasmid s
310	74.5	4.3	359	2	D89007	protein F59B1.6 [i	383	73	4.2	361	2	AG0169	pancreatic stone p
311	74.5	4.3	367	2	B97317	probable membrane	384	73	4.2	380	2	JN0594	phosphoserine tran
312	74.5	4.3	455	2	F96817	hypothetical prote	385	73	4.2	423	2	T19581	pectate lyase (EC
313	74.5	4.3	478	2	T21144	hypothetical prote	386	73	4.2	438	2	A32670	hypothetical prote
314	74.5	4.3	512	1	ALBSL	alpha-amylose (EC	387	73	4.2	441	2	JC7653	pectate lyase (EC
315	74.5	4.3	560	2	T16833	hypothetical prote	388	73	4.2	480	2	T04021	cellulase (EC 3.2.
316	74.5	4.3	640	2	JQ1584	genome polypotein	389	73	4.2	484	2	S66713	hypothetical prote
317	74.5	4.3	642	2	C96777	P25A4.24 [imported	390	73	4.2	496	2	AI2013	UDP-N-acetylmuramo
318	74.5	4.3	922	2	T37256	metalloproteinase	391	73	4.2	503	2	S31940	starch-degrading e
319	74.5	4.3	984	2	A39753	protein-tyrosine k	392	73	4.2	518	2	T05277	dihydrofolate redu
320	74.5	4.3	1161	2	S72645	pilYi protein - Ps	393	73	4.2	527	2	B70700	hypothetical prote
321	74.5	4.3	1280	2	T42514	kinase anchor prot	394	73	4.2	556	1	S31330	inulinase (EC 3.2.

395	73	4.2	564	1	HMIVF7	hemagglutinin prec
396	73	4.2	565	1	HMIVTN	hemagglutinin prec
397	73	4.2	617	2	S10511	thrombin (EC 3.4.2
398	73	4.2	627	2	S95107	choline binding pr
399	73	4.2	758	2	S30948	ferrichrome recept
400	73	4.2	762	2	JC7174	N,N-dimethylformam
401	73	4.2	939	2	T32521	hypothetical prote
402	73	4.2	1180	2	E86719	hypothetical prote
403	73	4.2	1217	2	S52714	sericin1B - silkwo
404	73	4.2	1239	1	VHVVBE	structural polypro
405	73	4.2	2187	2	S60224	polyketide synthas
406	72.5	4.1	189	2	B42514	H2R protein - vacc
407	72.5	4.1	206	2	S24400	insecticyanin A -
408	72.5	4.1	214	2	S44706	opacity protein op
409	72.5	4.1	282	2	F82748	hypothetical prote
410	72.5	4.1	298	2	G65006	hypothetical prote
411	72.5	4.1	339	2	G82864	hypothetical prote
412	72.5	4.1	445	2	T33617	hypothetical prote
413	72.5	4.1	512	2	TL3635	hypothetical prote
414	72.5	4.1	519	2	JC5926	probable minor str
415	72.5	4.1	562	2	A41707	secreted klotho pr
416	72.5	4.1	587	2	S36231	oligo-1,6-glucosid
417	72.5	4.1	590	2	T02096	beta-fructofuranos
418	72.5	4.1	617	2	E72803	probable beta-fruc
419	72.5	4.1	632	2	T02627	Gp31 protein - Myc
420	72.5	4.1	641	2	S41434	hypothetical prote
421	72.5	4.1	662	2	T48128	gene NS-1 protein
422	72.5	4.1	702	2	T12624	probable reverse t
423	72.5	4.1	752	2	S61505	NADH2 dehydrogenas
424	72.5	4.1	787	2	G64620	iron(III) dicitrat
425	72.5	4.1	804	2	T14762	hypothetical prote
426	72.5	4.1	818	2	T02231	hypothetical prote
427	72.5	4.1	934	2	T25864	probable isoamylas
428	72.5	4.1	1012	2	JC5925	hypothetical prote
429	72.5	4.1	1261	2	T50065	membrane klotho pr
430	72.5	4.1	1396	2	T10627	hypothetical prote
431	72.5	4.1	1422	2	T42636	hypothetical prote
432	72.5	4.1	1888	2	T14273	protein-tyrosine-p
433	72.5	4.1	2180	2	T29764	zinc finger protei
434	72.5	4.1	2214	2	T16305	hypothetical prote
435	72.5	4.1	2480	2	D84904	hypothetical prote
436	72.5	4.1	3133	2	S52093	hypothetical prote
437	72	4.1	282	2	H97226	hemocytin - silkwo
438	72	4.1	307	1	S53362	protein containing
439	72	4.1	308	2	T29754	hypothetical prote
440	72	4.1	309	2	G75286	hypothetical prote
441	72	4.1	329	2	S08627	serine proteinase
442	72	4.1	357	2	A95888	chitinase (EC 3.2.
443	72	4.1	400	2	T24258	probable ABC trans
444	72	4.1	402	1	JU0332	hypothetical prote
445	72	4.1	479	2	T40683	alkaline proteinas
446	72	4.1	491	2	T06798	cell cycle protein
447	72	4.1	496	2	T23565	probable starch sy
448	72	4.1	504	2	S12164	hypothetical prote
449	72	4.1	507	2	S56143	serralysin (EC 3.4
450	72	4.1	550	2	S65753	cell cycle protein
451	72	4.1	564	1	HMIVF1	beta-fructofuranos
452	72	4.1	564	1	HMIVF8	hemagglutinin prec
453	72	4.1	583	2	S01496	hemagglutinin prec
454	72	4.1	603	2	T22111	lamin B - African
455	72	4.1	627	2	G97975	hypothetical prote
456	72	4.1	722	2	T30995	hypothetical prote
457	72	4.1	767	2	T30018	hypothetical prote
458	72	4.1	780	1	WMBEH8	infected cell prot
459	72	4.1	815	2	JN0689	glutenin, high-mol
460	72	4.1	821	2	E87503	1,4-beta-D-glucan
461	72	4.1	836	1	S25218	outer membrane ush
462	72	4.1	937	2	A56517	nucleoporin Nup98
463	72	4.1	952	2	I50612	protein-tyrosine k
464	72	4.1	953	2	F96498	hypothetical prote
465	72	4.1	1144	2	A36968	pi-like adhesin pr
466	72	4.1	1250	2	T27706	hypothetical prote
467	72	4.1	1254	1	VHVVBE	structural polypro

541	71	4.1	561	2	G96752	unknown protein F2	614	70	4.0	295	2	A64756	attaching and effa
542	71	4.1	570	2	A45249	alpha-glucosidase	615	70	4.0	389	1	S39720	probable hydro-lysa
543	71	4.1	570	2	T32743	hypothetical prote	616	70	4.0	419	2	JC4522	alpha-galactosidas
544	71	4.1	574	2	T16230	hypothetical prote	617	70	4.0	430	2	S69913	hypertension-assoc
545	71	4.1	588	2	T26193	hypothetical prote	618	70	4.0	434	2	T32520	hypothetical prote
546	71	4.1	603	2	T03295	pyruvate decarboxy	619	70	4.0	462	4	S33798	FUS/CHOP mutant fu
547	71	4.1	627	2	B83692	hypothetical prote	620	70	4.0	468	2	T49682	hypothetical prote
548	71	4.1	654	2	AG0995	glycogen operon pr	621	70	4.0	471	2	C71439	hypothetical prote
549	71	4.1	657	2	E81901	probable phage tai	622	70	4.0	479	2	T05588	cellulase (EC 3.2.
550	71	4.1	681	2	E82812	outer membrane hem	623	70	4.0	483	2	T71439	probable Beta-Amyl
551	71	4.1	686	1	A59271	Ra-reactive factor	624	70	4.0	514	2	B64634	hypothetical prote
552	71	4.1	787	2	C84898	hypothetical prote	625	70	4.0	523	2	F86481	59.2K hypothetical
553	71	4.1	792	2	F71894	iron (III) dicitra	626	70	4.0	526	1	S33799	RNA-binding protei
554	71	4.1	833	1	A31593	heat shock transcr	627	70	4.0	527	2	E86432	Ts18.15 protein -
555	71	4.1	888	2	S28791	collagen alpha 1(X	628	70	4.0	531	2	T04722	hypothetical prote
556	71	4.1	906	2	G90281	conserved hypothet	629	70	4.0	548	2	B87596	xylosidase/arabino
557	71	4.1	919	2	T16693	hypothetical prote	630	70	4.0	552	2	JC7666	serine-type carbox
558	71	4.1	957	2	A84089	hypothetical prote	631	70	4.0	553	2	C84920	hypothetical prote
559	71	4.1	1060	2	T31763	hypothetical prote	632	70	4.0	564	1	HMIVF4	hemagglutinin prec
560	71	4.1	1230	2	T17187	CL3AB protein - ra	633	70	4.0	566	1	HYBSU	bacillolysin (EC 3
561	71	4.1	1273	2	T17188	CL3AC protein - ra	634	70	4.0	575	1	S03745	beta-amylase (EC 3
562	71	4.1	1274	2	T10729	transferrin-like p	635	70	4.0	583	2	S30930	catechol oxidase (
563	71	4.1	1298	2	T17199	CL3BB protein - ra	636	70	4.0	585	2	C49596	genome polyprotein
564	71	4.1	1341	2	T17200	CL3BC protein - ra	637	70	4.0	591	2	S33542	catechol oxidase (
565	71	4.1	1459	2	T17186	CL3AA protein - ra	638	70	4.0	600	2	B86854	hypothetical prote
566	71	4.1	1508	2	T31098	probable dextranau	639	70	4.0	638	2	B83890	hypothetical prote
567	71	4.1	1518	2	D96660	protein F2K11.14 [	640	70	4.0	686	2	S28042	hemin receptor pre
568	71	4.1	1527	2	T17198	CL3BA protein - ra	641	70	4.0	701	2	T13587	NADH2 dehydrogenas
569	71	4.1	1548	2	S34583	serine proteinase	642	70	4.0	738	2	S14270	alcohol dehydrogen
570	71	4.1	1550	2	T14327	alpha-latrotoxin r	643	70	4.0	738	2	T00748	4-alpha-glucanotra
571	71	4.1	1705	2	F71413	hypothetical prote	644	70	4.0	757	2	C70034	conserved hypothet
572	71	4.1	3010	1	A45573	genome polyprotein	645	70	4.0	761	2	AI0074	probable autotrans
573	70.5	4.0	248	2	T04758	hypothetical prote	646	70	4.0	819	2	A13197	TonB-dependent rec
574	70.5	4.0	285	2	D90010	conserved hypothet	647	70	4.0	822	2	AB0238	heamin storage sys
575	70.5	4.0	314	2	JH0389	pectin lyase (EC 4	648	70	4.0	822	2	T47007	hypothetical prote
576	70.5	4.0	365	1	MBPFP2	outer membrane por	649	70	4.0	879	2	F85875	probable fimbrial
577	70.5	4.0	373	1	AJRTQ	glutamate-ammonia	650	70	4.0	879	2	E91031	probable outer mem
578	70.5	4.0	399	1	S35719	transcription fact	651	70	4.0	929	2	T08658	hypothetical prote
579	70.5	4.0	484	2	JU0091	sucrose alpha-gluc	652	70	4.0	1291	2	T13389	hypothetical prote
580	70.5	4.0	510	2	AF1182	oligo-1,6-glucosid	653	70	4.0	1417	2	H90670	probable invasini
581	70.5	4.0	525	1	K87HGH	histidine-rich gly	654	70	4.0	1417	2	D85521	probable adhesin e
582	70.5	4.0	559	2	H83758	alpha, alpha-phosph	655	70	4.0	1545	2	B41859	IGA-specific metal
583	70.5	4.0	566	2	S69887	hemagglutinin prec	656	70	4.0	1569	2	A65044	hypothetical prote
584	70.5	4.0	594	2	E96667	unknown protein, 6	657	70	4.0	2233	2	T28669	surface protein 51
585	70.5	4.0	605	2	T15291	spingomyelin phos	658	70	4.0	3010	1	GNWVTC	genome polyprotein
586	70.5	4.0	614	2	S57821	pyruvate decarboxy	659	69.5	4.0	168	2	PN0680	nitrogenase (EC 1.
587	70.5	4.0	639	2	JQ0607	glucan 1,4-alpha-g	660	69.5	4.0	189	1	QQVZH2	H2 protein - vacci
588	70.5	4.0	642	1	S52111	uromodulin precurs	661	69.5	4.0	276	2	T09131	chitinase (EC 3.2.
589	70.5	4.0	649	2	T32668	hypothetical prote	662	69.5	4.0	314	2	C64045	2-dehydro-3-deoxyg
590	70.5	4.0	653	2	F85620	partial fimbrial u	663	69.5	4.0	323	2	JC5691	cysteine proteinase
591	70.5	4.0	653	2	H90756	partial fimbrial u	664	69.5	4.0	373	1	AJHUQ	glutamate-ammonia
592	70.5	4.0	686	2	A55665	microtubule-associ	665	69.5	4.0	374	2	AO0149	outer membrane pro
593	70.5	4.0	695	2	T13639	probable tail-host	666	69.5	4.0	390	2	T39818	hypothetical prote
594	70.5	4.0	712	2	F97012	hypothetical prote	667	69.5	4.0	401	2	S65138	glycoprotein antiq
595	70.5	4.0	746	2	A97979	competence protein	668	69.5	4.0	427	2	S74211	PAS-6/7 protein pr
596	70.5	4.0	793	2	H82594	ferric enterobacti	669	69.5	4.0	448	2	JW0037	beta-glucosidase (
597	70.5	4.0	812	2	AG3138	fimbrial usher pro	670	69.5	4.0	449	1	NSHUHS	complement factor
598	70.5	4.0	812	2	D98149	hypothetical prote	671	69.5	4.0	453	2	D69828	conserved hypothet
599	70.5	4.0	817	2	D87390	TonB-dependent rec	672	69.5	4.0	454	2	T43069	probable serine pr
600	70.5	4.0	833	2	H95029	leucyl-tRNA synthe	673	69.5	4.0	455	2	G71896	probable outer mem
601	70.5	4.0	935	2	T21773	hypothetical prote	674	69.5	4.0	477	2	J80597	t-plasminogen acti
602	70.5	4.0	927	2	T21772	hypothetical prote	675	69.5	4.0	497	2	G86299	F309.24 protein -
603	70.5	4.0	944	2	C81798	lactoferrin bindin	676	69.5	4.0	528	2	S38242	hypothetical prote
604	70.5	4.0	995	2	A56599	embryo kinase 5 -	677	69.5	4.0	545	1	B39827	4-coumarate-CoA li
605	70.5	4.0	997	2	S73556	MG414 homolog C12	678	69.5	4.0	555	1	S17502	inulinase (EC 3.2.
606	70.5	4.0	1034	2	JC2143	ice nucleation act	679	69.5	4.0	585	2	T19814	hypothetical prote
607	70.5	4.0	1051	2	D82428	chitodextrinase VC	680	69.5	4.0	595	2	AG3194	alpha-amylase Atu5
608	70.5	4.0	1138	2	H86201	hypothetical prote	681	69.5	4.0	598	2	B75626	PTS system, fructo
609	70.5	4.0	1260	2	H89984	hypothetical prote	682	69.5	4.0	602	2	S71557	pyruvate decarboxy
610	70.5	4.0	1528	2	D85912	hypothetical prote	683	69.5	4.0	611	1	S06047	endo-1,4-beta-xyta
611	70.5	4.0	1571	2	C91068	hypothetical prote	684	69.5	4.0	642	2	B72428	laminarinase - The
612	70.5	4.0	1711	2	T31337	1,4-beta-glucanase	685	69.5	4.0	673	2	AF0232	pesticin/yeriniab
613	70	4.0	271	2	S72382	hypothetical prote	686	69.5	4.0	673	2	A56148	pesticin receptor

687	69.5	4.0	702	1	A48562	coat protein - San	760	69	3.9	3990	2	C89921	hypothetical prote
688	69.5	4.0	720	2	AH0117	ornithine decarbox	761	68.5	3.9	183	2	AI3566	hypothetical prote
689	69.5	4.0	728	2	AF0995	1,4-alpha-glucan b	762	68.5	3.9	206	2	T12743	hypothetical prote
690	69.5	4.0	738	2	AF0995	dipeptidyl peptida	763	68.5	3.9	219	2	T21736	hypothetical prote
691	69.5	4.0	746	2	C95110	competence protein	764	68.5	3.9	231	2	AI0372	hypothetical prote
692	69.5	4.0	776	2	S45495	isp4 protein - fis	765	68.5	3.9	245	2	E86450	hypothetical prote
693	69.5	4.0	797	1	VBEX1	glycoprotein X pre	766	68.5	3.9	256	2	S77522	hypothetical prote
694	69.5	4.0	804	2	G75125	hypothetical prote	767	68.5	3.9	259	2	A29831	heat-labile entero
695	69.5	4.0	840	2	G98169	hypothetical prote	768	68.5	3.9	263	2	S72528	chitinase (EC 3.2.
696	69.5	4.0	840	2	AF3117	hypothetical prote	769	68.5	3.9	275	2	T51651	myb-related trans
697	69.5	4.0	866	2	T45462	hypothetical prote	770	68.5	3.9	306	2	G84729	hypothetical prote
698	69.5	4.0	1063	2	T00624	membrane glycoprot	771	68.5	3.9	310	2	C86475	unknown protein, 4
699	69.5	4.0	1170	2	A40558	endo-1,4-beta-xyla	772	68.5	3.9	323	2	T05694	pathogenesis-relat
700	69.5	4.0	1224	1	ERHUAH	thrombospondin 1 p	773	68.5	3.9	328	2	S47047	drdp-4-dehydroram
701	69.5	4.0	1231	1	ERHUAH	coatomer complex a	774	68.5	3.9	366	1	W2WLR1	E2 protein - rhesu
702	69.5	4.0	1365	2	A14883	complement factor	775	68.5	3.9	373	2	S41452	glutamate-ammonia
703	69.5	4.0	1475	2	B33135	glucosyltransferas	776	68.5	3.9	386	2	S72435	RNA-binding protei
704	69.5	4.0	1520	1	TVFFA	gtfB protein precu	777	68.5	3.9	396	1	S15992	flavohemoglobin hm
705	69.5	4.0	1561	2	S61314	protein-tyrosine k	778	68.5	3.9	396	2	P85900	dihydropteridine r
706	69.5	4.0	1748	2	S42136	IgA-specific metal	779	68.5	3.9	413	2	D86920	dihydropteridine r
707	69.5	4.0	3002	2	A47221	cnjB protein - tet	780	68.5	3.9	440	2	AB1111	probable UDP-galac
708	69	3.9	125	2	PH0957	fibrillin 1 precu	781	68.5	3.9	465	1	T51095	B. subtilis yycH p
709	69	3.9	172	2	S75094	Ig heavy chain v r	782	68.5	3.9	467	1	PABYCC	acid phosphatase (
710	69	3.9	233	2	S36350	hypothetical prote	783	68.5	3.9	486	2	F84686	hypothetical prote
711	69	3.9	246	2	AI1625	opacity protein op	784	68.5	3.9	513	2	S63701	bifunctional cellu
712	69	3.9	253	2	JC5014	hypothetical prote	785	68.5	3.9	534	2	A29776	mannosyl-oligosacc
713	69	3.9	275	2	T03032	2,4-dichlorophenol	786	68.5	3.9	546	2	JC4113	glucan 1,4-alpha-g
714	69	3.9	288	2	T14863	chitinase (EC 3.2.	787	68.5	3.9	546	2	S72176	neutral proteinase
715	69	3.9	305	2	S73645	porin Mip1 - Norwa	788	68.5	3.9	597	2	T07096	thermolysin (EC 3.
716	69	3.9	307	2	T38206	probable lipoprote	789	68.5	3.9	609	2	S57378	hypothetical prote
717	69	3.9	311	2	E96714	probable phosphopr	790	68.5	3.9	611	2	G83177	probable sodium/hy
718	69	3.9	380	2	A53809	probable DNA-bindi	791	68.5	3.9	640	1	ALASGR	hypothetical prote
719	69	3.9	397	2	A97197	mitochondrial resp	792	68.5	3.9	641	2	S41439	glucan 1,4-alpha-g
720	69	3.9	398	2	JQ0366	transglutaminase-1	793	68.5	3.9	661	1	S59633	gene NS-1 protein
721	69	3.9	399	1	D69056	phospholipase C (E	794	68.5	3.9	680	2	S60142	hypothetical prote
722	69	3.9	402	2	T02378	conserved hypotet	795	68.5	3.9	687	2	S43587	endo-1,4-beta-xyla
723	69	3.9	416	2	F72840	hypothetical prote	796	68.5	3.9	692	2	F98114	outer membrane pro
724	69	3.9	418	2	H95407	hypothetical prote	797	68.5	3.9	698	2	G83443	F26F3.2 protein (c
725	69	3.9	419	1	S25835	probable aminometh	798	68.5	3.9	702	2	A69222	cholesterol-binding pr
726	69	3.9	431	2	T29850	subtilisin (EC 3.4	799	68.5	3.9	721	2	B83237	NADH2 dehydrogenas
727	69	3.9	432	2	A12613	hypothetical prote	800	68.5	3.9	742	2	T25415	hypothetical prote
728	69	3.9	432	2	G97395	hypothetical prote	801	68.5	3.9	802	2	B81794	probable TonB-depe
729	69	3.9	432	2	D87649	hypothetical prote	802	68.5	3.9	839	2	D97013	hypothetical prote
730	69	3.9	443	2	E65008	tolB protein [impo	803	68.5	3.9	853	2	T07036	probably secreted
731	69	3.9	444	2	D26421	shufflon B' - Each	804	68.5	3.9	926	2	D86897	lipoxigenase (EC 1
732	69	3.9	453	2	S49168	beta tubulin 1 - r	805	68.5	3.9	938	2	AF1772	hypothetical prote
733	69	3.9	455	2	B64860	hypothetical prote	806	68.5	3.9	985	2	DC7789	internalin-like pr
734	69	3.9	461	1	KFHU	ymfN protein - Esc	807	68.5	3.9	1050	2	J87889	pyruvate dehydroge
735	69	3.9	522	2	T18504	coagulation factor	808	68.5	3.9	1057	2	T15720	heparinase (EC 3.2
736	69	3.9	527	2	S49814	hypothetical prote	809	68.5	3.9	1210	2	A25547	hypothetical prote
737	69	3.9	547	2	A56740	transferrin-bindin	810	68.5	3.9	1453	2	S41453	ice nucleation pro
738	69	3.9	579	2	H90551	sperm-egg recognit	811	68.5	3.9	1455	1	A48925	spike protein - ca
739	69	3.9	617	2	G01205	lipoprotein [impor	812	68.5	3.9	1529	2	S69688	mannose receptor p
740	69	3.9	645	2	G01205	TYL protein - huma	813	68.5	3.9	1684	2	T02367	hypothetical prote
741	69	3.9	655	1	A46688	hepatocyte growth	814	68.5	3.9	1876	2	S50235	1,3-beta-glucan sy
742	69	3.9	682	2	F81332	probable periplasm	815	68.5	3.9	2871	2	A55567	fibrillin 1 - bovi
743	69	3.9	699	2	A54767	transcription fact	816	68.5	3.9	2971	2	S58870	reelin precursor -
744	69	3.9	769	2	H97033	alpha-glucosidase	817	68.5	3.9	3461	2	E86468	zonadhesin - mouse
745	69	3.9	784	2	E82731	outer membrane ant	818	68.5	3.9	3576	2	T42215	hypothetical prote
746	69	3.9	803	2	F83360	glucose dehydrogen	819	68.5	3.9	3576	2	E86468	probable periplasm
747	69	3.9	889	2	B55123	coatomer complex b	820	68.5	3.9	3576	2	E86468	probable periplasm
748	69	3.9	890	2	A30481	bacteriocin BCNS -	821	68.5	3.9	3576	2	E86468	probable periplasm
749	69	3.9	961	2	AD0548	putative autotransp	822	68.5	3.9	3576	2	E86468	probable periplasm
750	69	3.9	1021	2	I40805	collagenase - Clos	823	68.5	3.9	3576	2	E86468	probable periplasm
751	69	3.9	1098	2	T28816	hypothetical prote	824	68.5	3.9	3576	2	E86468	probable periplasm
752	69	3.9	1207	2	T37554	hypothetical prote	825	68.5	3.9	3576	2	E86468	probable periplasm
753	69	3.9	1335	2	T30211	autolysin E - Strap	826	68.5	3.9	3576	2	E86468	probable periplasm
754	69	3.9	1390	2	T30346	protein C37C3.6a (	827	68.5	3.9	3576	2	E86468	probable periplasm
755	69	3.9	1558	2	C89114	peptidoglycan boun	828	68.5	3.9	3576	2	E86468	probable periplasm
756	69	3.9	1578	2	AD1512	hypothetical prote	829	68.5	3.9	3576	2	E86468	probable periplasm
757	69	3.9	2167	2	T34395	hypothetical prote	830	68.5	3.9	3576	2	E86468	probable periplasm
758	69	3.9	2295	2	AE0074	probable adhesin y	831	68.5	3.9	3576	2	E86468	probable periplasm
759	69	3.9	3432	1	GNWVJS	genome polyprotein	832	68.5	3.9	3576	2	E86468	probable periplasm
			3432	1	GNWVJS	genome polyprotein	833	68.5	3.9	3576	2	E86468	probable periplasm

833	68	3.9	389	2	E86634	hypothetical prote	906	67.5	3.9	498	2	H85190	probable beta-amy
834	68	3.9	398	2	B49231	phospholipase C, a	907	67.5	3.9	544	2	A42464	microbial metallo
835	68	3.9	407	2	E88976	protein F54E2.1 [i	908	67.5	3.9	547	2	A32803	glucan 1,4-alpha-m
836	68	3.9	417	1	A39904	gastric intrinsic	909	67.5	3.9	548	2	T52556	beta-amyase [EC 3
837	68	3.9	417	2	AB2359	hypothetical prote	910	67.5	3.9	552	2	S19134	probable alpha-glu
838	68	3.9	425	2	C89753	protein Fl1C7.3 [i	911	67.5	3.9	552	2	AH1915	hypothetical prote
839	68	3.9	439	2	G84432	probable C2H2-type	912	67.5	3.9	566	1	HMIV	hemagglutinin prec
840	68	3.9	440	2	T00583	probable indole-3-	913	67.5	3.9	571	2	C75174	glycyl-L-tryptoph
841	68	3.9	453	2	C86727	beta-glucosidase [	914	67.5	3.9	599	2	G83296	hypothetical prote
842	68	3.9	457	2	T23494	phenylalanine 4-mo	915	67.5	3.9	607	2	S69522	probable terminase
843	68	3.9	469	2	S45453	alpha-galactosidas	916	67.5	3.9	616	2	JC7905	fructan 6-fructosy
844	68	3.9	470	1	NM1VW8	exo-alpha-sialidas	917	67.5	3.9	648	1	JQ1150	protein kinase (EC
845	68	3.9	475	2	T16364	hypothetical prote	918	67.5	3.9	676	2	F91185	alpha-amyase [imp
846	68	3.9	491	2	T21421	hypothetical prote	919	67.5	3.9	676	2	D86032	alpha-amyase [imp
847	68	3.9	503	2	B97262	N-terminal domain	920	67.5	3.9	677	1	S41022	hypothetical prote
848	68	3.9	514	2	E71880	probable outer mem	921	67.5	3.9	677	1	S09078	chromogranin B pre
849	68	3.9	529	2	AC2112	hypothetical prote	922	67.5	3.9	680	2	JC5133	protein-glutamine
850	68	3.9	532	1	CPBYX	carboxypeptidase C	923	67.5	3.9	691	2	C64548	outer membrane pro
851	68	3.9	564	1	HM1VF3	hemagglutinin prec	924	67.5	3.9	693	2	A45991	protein-glutamine
852	68	3.9	588	2	S34786	catechol oxidase (	925	67.5	3.9	702	2	T13058	NADH2 dehydrogenas
853	68	3.9	591	1	F0VMM	gag polyprotein -	926	67.5	3.9	720	2	F64079	ornithine decarbox
854	68	3.9	639	2	JT0479	glucan 1,4-alpha-g	927	67.5	3.9	730	1	S24124	trimethylamine deh
855	68	3.9	672	1	S73715	cytadherence acces	928	67.5	3.9	737	2	S28030	DNA-binding protei
856	68	3.9	686	2	T06334	1,4-alpha-glucan b	929	67.5	3.9	771	2	JC7388	M83 protein - huma
857	68	3.9	713	2	T21201	hypothetical prote	930	67.5	3.9	792	2	D95351	VirB4 type IV secr
858	68	3.9	726	2	T31287	hypothetical prote	931	67.5	3.9	794	1	TLBPB7	tail tubular prote
859	68	3.9	752	2	E72616	hypothetical prote	932	67.5	3.9	798	2	F69549	acetyl-CoA decarbo
860	68	3.9	753	2	D83081	probable outer mem	933	67.5	3.9	798	2	S09867	hypothetical prote
861	68	3.9	773	2	A83888	hypothetical prote	934	67.5	3.9	867	2	D87320	hypothetical prote
862	68	3.9	790	2	T47959	hypothetical prote	935	67.5	3.9	940	2	S37216	hexon protein - hu
863	68	3.9	815	2	T19704	hypothetical prote	936	67.5	3.9	962	2	S03818	carboxymethylcellu
864	68	3.9	856	2	T00349	Avicelase III - As	937	67.5	3.9	964	2	H89582	protein K07E3.6 [i
865	68	3.9	884	2	H83322	hypothetical prote	938	67.5	3.9	966	2	A33626	fibrinogen alpha c
866	68	3.9	943	2	G81070	lactoferrin-bindin	939	67.5	3.9	989	2	C83035	hypothetical prote
867	68	3.9	943	2	T35497	hypothetical prote	940	67.5	3.9	1034	2	JC5569	serine proteinase
868	68	3.9	960	2	JE0356	gamma-aminobutyric	941	67.5	3.9	1036	2	E70697	probable arabinosy
869	68	3.9	1144	2	A54810	TMV resistance pro	942	67.5	3.9	1094	2	JC5568	RNA-directed RNA p
870	68	3.9	1300	2	A36502	insulin receptor-r	943	67.5	3.9	1116	2	T30828	hypothetical prote
871	68	3.9	1347	2	T30909	endo-1,4-beta-xyla	944	67.5	3.9	1227	2	T48028	latrophilin-3, spl
872	68	3.9	1377	2	I54632	tsh protein - Esch	945	67.5	3.9	1231	2	T18390	latrophilin-3, spl
873	68	3.9	1395	2	T00068	hypothetical prote	946	67.5	3.9	1240	2	T18393	latrophilin-3, spl
874	68	3.9	1878	2	E86189	hypothetical prote	947	67.5	3.9	1274	2	T18391	latrophilin-3, spl
875	68	3.9	1906	2	AD2443	hypothetical prote	948	67.5	3.9	1283	2	T18394	latrophilin-3, spl
876	68	3.9	2161	2	JH0564	calcium channel al	949	67.5	3.9	1290	2	A57190	ebnerin precursor
877	68	3.9	2181	2	A31918	calcium channel al	950	67.5	3.9	1299	2	T18398	latrophilin-3, spl
878	68	3.9	2203	2	T42742	voltage-dependen	951	67.5	3.9	1308	2	T18408	latrophilin-3, spl
879	68	3.9	2269	1	JQ1750	genome polyprotein	952	67.5	3.9	1329	2	T29074	hypothetical prote
880	68	3.9	2893	2	A64556	toxin-like outer m	953	67.5	3.9	1342	2	T18405	latrophilin-3, spl
881	68	3.9	3010	1	S18030	genome polyprotein	954	67.5	3.9	1351	2	T18409	latrophilin-3, spl
882	67.5	3.9	136	2	PH0960	Ig heavy chain V r	955	67.5	3.9	1361	2	T29435	frazzled gene prot
883	67.5	3.9	246	2	AG1263	hypothetical prote	956	67.5	3.9	1375	2	T13822	frazzled gene prot
884	67.5	3.9	250	2	T43153	probable aldehyde	957	67.5	3.9	1444	2	T18856	angiogenesis inhib
885	67.5	3.9	281	2	F86355	T16E15.10 protein	958	67.5	3.9	1503	2	T18389	latrophilin-3, spl
886	67.5	3.9	313	2	T02534	hypothetical prote	959	67.5	3.9	1512	2	T18392	latrophilin-3, spl
887	67.5	3.9	314	2	AD0220	flagellar protein	960	67.5	3.9	1526	2	T13823	frazzled gene prot
888	67.5	3.9	316	2	G86333	hypothetical prote	961	67.5	3.9	1530	2	AH1396	peptidoglycan anch
889	67.5	3.9	350	2	A82299	outer membrane pro	962	67.5	3.9	1537	2	JC4172	DNA (cytosine-5-)
890	67.5	3.9	360	2	T35783	probable secreted	963	67.5	3.9	1571	2	T18395	latrophilin-3, spl
891	67.5	3.9	369	2	S70847	outer membrane por	964	67.5	3.9	1580	2	T18407	latrophilin-3, spl
892	67.5	3.9	372	2	T06661	hypothetical prote	965	67.5	3.9	1844	2	T51890	related to Nup98-N
893	67.5	3.9	377	2	T00152	hypothetical prote	966	67.5	3.9	2013	2	AD1129	probable peptidogl
894	67.5	3.9	386	2	S48755	major surface prot	967	67.5	3.9	2334	2	S32920	cell wall-associat
895	67.5	3.9	390	2	H86253	hypothetical prote	968	67.5	3.9	4976	2	T14165	peptide synthetase
896	67.5	3.9	392	2	I51422	glutamine syntheta	969	67.5	3.8	133	2	A47267	botrocetin alpha c
897	67.5	3.9	420	2	D95972	probable sugar upt	970	67.5	3.8	197	1	A44597	endo-1,4-beta-xyla
898	67.5	3.9	428	2	G89982	hypothetical prote	971	67.5	3.8	204	2	T28985	hypothetical prote
899	67.5	3.9	449	2	S16748	proline-rich prote	972	67.5	3.8	264	2	T40927	hypothetical wfl1
900	67.5	3.9	458	2	T36442	probable serine pr	973	67.5	3.8	273	2	E81330	probable periplasm
901	67.5	3.9	460	2	JN0663	alpha-amyase (EC	974	67.5	3.8	288	2	T22721	hypothetical prote
902	67.5	3.9	467	1	L1DG	triacylglycerol li	975	67.5	3.8	319	2	T32435	hypothetical prote
903	67.5	3.9	484	2	H95200	sucrose-6-phosphat	976	67.5	3.8	340	2	C71266	conserved hypothet
904	67.5	3.9	484	2	F98067	beta-fructofuranos	977	67.5	3.8	361	1	XNEBPY	phosphoserine tran
905	67.5	3.9	494	2	A89985	hypothetical prote	978	67.5	3.8	364	2	T25124	hypothetical prote

979	67	3.8	366	2	B69949	phage-related prot	1052	66.5	3.8	418	2	P95245	tyrosyl-tRNA synth
980	67	3.8	375	2	A46174	RNA-binding protei	1053	66.5	3.8	437	2	H69952	hypothetical prote
981	67	3.8	392	2	S72436	RNA-binding protei	1054	66.5	3.8	456	2	S61971	hypothetical prote
982	67	3.8	396	2	T27946	hypothetical prote	1055	66.5	3.8	463	2	A44808	cellulase (EC 3.2.
983	67	3.8	397	2	I39507	kappa-carragehase	1056	66.5	3.8	477	1	KCHUS1	stromelysin 1 (EC
984	67	3.8	398	2	A30565	phospholipase C (E	1057	66.5	3.8	519	2	E84539	dihydrofolate redu
985	67	3.8	420	2	AH2711	3-oxoacyl-(acyl ca	1058	66.5	3.8	525	2	C98183	mannotol 2-dehydro
986	67	3.8	427	2	T04823	hypothetical prote	1059	66.5	3.8	528	1	PARU1	alkaline phosphata
987	67	3.8	432	1	FLMGS	fibrinogen gamma C	1060	66.5	3.8	548	2	C82698	electron transfer
988	67	3.8	437	1	T49034	acid phosphatase (	1061	66.5	3.8	564	2	T41503	alpha-amylase - fi
989	67	3.8	437	2	S67679	probable membrane	1062	66.5	3.8	579	2	S33759	alpha,alpha-trehal
990	67	3.8	441	2	S60247	platelet-activatin	1063	66.5	3.8	600	2	T46880	succinate dehydrog
991	67	3.8	442	2	F97493	3-oxoacyl-acyl car	1064	66.5	3.8	633	2	A75069	dipeptide transpor
992	67	3.8	448	2	JW0038	beta-glucosidase (	1065	66.5	3.8	642	2	A96560	hypothetical prote
993	67	3.8	471	2	S50310	alpha-galactosidas	1066	66.5	3.8	663	1	Q8ECIC	colicin I receptor
994	67	3.8	484	2	A83082	probable porin PA4	1067	66.5	3.8	683	2	S01433	repressor protein
995	67	3.8	496	2	JC5110	cyclin-dependent k	1068	66.5	3.8	705	2	T01730	hypothetical prote
996	67	3.8	499	2	S04856	chitinase (EC 3.2.	1069	66.5	3.8	714	2	D85014	hypothetical prote
997	67	3.8	509	2	A84404	hypothetical prote	1070	66.5	3.8	730	2	B87266	TonB-dependent rec
998	67	3.8	512	2	T13330	hypothetical prote	1071	66.5	3.8	767	2	C71909	iron (III) diglita
999	67	3.8	551	2	A83889	hypothetical prote	1072	66.5	3.8	783	2	E89551	probable low-affin
1000	67	3.8	555	2	C97612	hypothetical prote	1073	66.5	3.8	796	2	T37330	glucan endo-1,3-be
1001	67	3.8	560	1	HMTVTM	hemagglutinin prec	1074	66.5	3.8	877	2	JN0772	aconitase XF0290 [
1002	67	3.8	564	1	HMTVF6	hemagglutinin prec	1075	66.5	3.8	908	2	G82824	probable outer mem
1003	67	3.8	598	2	AG0890	probable arylsulfa	1076	66.5	3.8	970	2	F87450	TonB-dependent rec
1004	67	3.8	634	2	T18711	hypothetical prote	1077	66.5	3.8	1016	2	H71460	ras GTPase-activat
1005	67	3.8	634	2	T18702	hypothetical prote	1078	66.5	3.8	1137	2	D89610	hypothetical prote
1006	67	3.8	651	2	E86242	hypothetical prote	1079	66.5	3.8	1206	2	A64207	ras GTPase-activat
1007	67	3.8	656	2	T03473	acetate-CoA ligase	1080	66.5	3.8	1259	2	T19043	neural cell adhesi
1008	67	3.8	683	2	AG0217	oligopeptidase B (	1081	66.5	3.8	1265	1	A37967	TagA-related prote
1009	67	3.8	693	2	AB0969	ATP-dependent subC	1082	66.5	3.8	1335	2	A82494	hypothetical prote
1010	67	3.8	694	2	JC5554	complement subcomp	1083	66.5	3.8	1377	2	D90538	probable membrane
1011	67	3.8	699	2	H71005	hypothetical prote	1084	66.5	3.8	1609	2	S25345	hypothetical prote
1012	67	3.8	702	2	H71005	arylphorin precurs	1085	66.5	3.8	1619	2	S67083	hypothetical prote
1013	67	3.8	712	2	A61619	threonine-CrNA lig	1086	66.5	3.8	1829	2	T14280	RMI protein - mous
1014	67	3.8	714	1	YSHUT	ribonucleoside-dip	1087	66.5	3.8	1876	2	C70749	probable ppaA prot
1015	67	3.8	745	2	D65047	subtilisin-like pr	1088	66.5	3.8	1928	2	JS0610	beta-galactosidase
1016	67	3.8	764	2	S48521	AKR1 protein - yea	1089	66.5	3.8	2013	2	AI1489	probable peptidogl
1017	67	3.8	788	2	S53923	probable membrane	1090	66.5	3.8	2168	2	D88131	protein F10G7.10 [
1018	67	3.8	931	2	A49737	dipeptidyl aminope	1091	66	3.8	126	2	PH1418	Ig heavy chain V r
1019	67	3.8	983	2	A81723	polymorphic membra	1092	66	3.8	167	2	AH2963	conserved hypotet
1020	67	3.8	1217	2	F97177	alpha-glucosidase	1093	66	3.8	173	2	E98319	hypothetical prote
1021	67	3.8	1376	2	S63986	collagen alpha 5 c	1094	66	3.8	197	2	S25088	dehydrin DNM1 - ga
1022	67	3.8	1388	2	T00063	hypothetical prote	1095	66	3.8	215	2	JC1231	beta-crystallin A3
1023	67	3.8	1451	2	D64203	DNA polymerase III	1096	66	3.8	227	2	S43919	endo-1,4-beta-xyla
1024	67	3.8	2014	2	T21560	hypothetical prote	1097	66	3.8	248	2	PL0038	opacity protein D
1025	66.5	3.8	191	2	G90966	hypothetical prote	1098	66	3.8	253	2	A71648	pseudouridylate sy
1026	66.5	3.8	202	2	S35259	pyruvate decarboxy	1099	66	3.8	259	2	T14722	hypothetical prote
1027	66.5	3.8	205	2	T04370	perml protein - ba	1100	66	3.8	264	2	T46335	hypothetical prote
1028	66.5	3.8	257	2	AB2159	glucose-1-P cytidy	1101	66	3.8	286	2	T02119	probable DnaJ prot
1029	66.5	3.8	281	2	T31741	hypothetical prote	1102	66	3.8	299	2	S32896	hypothetical prote
1030	66.5	3.8	282	2	T50660	alpha-expansin 2 [	1103	66	3.8	314	2	T46276	hypothetical prote
1031	66.5	3.8	270	1	A64367	pyruvate synthase	1104	66	3.8	346	2	T20620	glutamyl endopepti
1032	66.5	3.8	277	2	S65069	chitinase (EC 3.2.	1105	66	3.8	357	1	S33321	probable p-loop AT
1033	66.5	3.8	278	2	S39310	merozoite surface	1106	66	3.8	370	2	S61058	glutamate-ammonia
1034	66.5	3.8	311	2	C89968	leukotoxin LukG [i	1107	66	3.8	377	2	JC7535	chitinase (EC 3.2.
1035	66.5	3.8	319	2	T17438	protein regulator	1108	66	3.8	405	2	G75027	alanyl-tRNA synthet
1036	66.5	3.8	319	2	AD0233	transcription regu	1109	66	3.8	416	2	D83370	probable porin PA2
1037	66.5	3.8	354	2	T05975	probable carboxy-t	1110	66	3.8	422	2	H70481	hypothetical prote
1038	66.5	3.8	359	2	F72418	basic membrane pro	1111	66	3.8	428	2	A81705	hemolysin homolog
1039	66.5	3.8	362	2	A38135	ADP-ribosylarginin	1112	66	3.8	433	2	T48118	peptide ABC transp
1040	66.5	3.8	367	2	T00086	rgpAc protein - St	1113	66	3.8	440	2	G90936	hypothetical prote
1041	66.5	3.8	370	2	H83541	probable periplasm	1114	66	3.8	445	2	A27263	probable thiosulfa
1042	66.5	3.8	372	2	A39293	probable oxidoredu	1115	66	3.8	485	2	C85785	50K epicle matrix
1043	66.5	3.8	375	2	T19273	cytotoxic granule-	1116	66	3.8	489	2	S67772	B-selectin - bovin
1044	66.5	3.8	378	2	A39293	probable alpha-1,2	1117	66	3.8	495	2	JC6141	beta 1,3-glucanase
1045	66.5	3.8	398	2	F75417	L-sorbose dehydr	1118	66	3.8	503	2	T39216	aldehyde dehydrog
1046	66.5	3.8	399	1	AJFFILM	glutamate-ammonia	1119	66	3.8	503	2	AC2446	hypothetical prote
1047	66.5	3.8	400	2	A42237	fork head domain p	1120	66	3.8	516	2	JB0134	cysteine proteinas
1048	66.5	3.8	400	2	A46297	beta-1,6-N-acetylgl	1121	66	3.8	527	2	A81712	mannan endo-1,4-be
1049	66.5	3.8	402	2	H86249	hypothetical prote	1122	66	3.8				
1050	66.5	3.8	405	2	A41734	beta-galactoside a	1123	66	3.8				
1051	66.5	3.8	418	2	C98110	tyrosine-tRNA liga	1124	66	3.8				

1125	66	3.8	527	2	T39927	probable serine-ri	1198	65.5	3.7	360	2	S00834	int-1-like protein
1126	66	3.8	529	2	T35966	probable secreted	1199	65.5	3.7	363	2	S08356	hypothetical prote
1127	66	3.8	530	2	JC7979	cellobiohydrolase	1200	65.5	3.7	365	2	JC4027	glutamate-ammonia
1128	66	3.8	532	2	A82551	phage-related port	1201	65.5	3.7	367	1	S62746	alcohol dehydrogen
1129	66	3.8	539	2	C90789	hemolysin activato	1202	65.5	3.7	397	2	JW0075	cysteine-dependent
1130	66	3.8	539	2	F85649	hemolysin activato	1203	65.5	3.7	405	2	T35117	probable secreted
1131	66	3.8	555	2	T06491	beta-fructofuranos	1204	65.5	3.7	406	2	T36632	probable oxidoredu
1132	66	3.8	556	2	T39479	probable serine-ri	1205	65.5	3.7	410	2	G81651	conserved hypothet
1133	66	3.8	574	2	T40213	hypothetical prote	1206	65.5	3.7	417	2	A96610	probable pectinace
1134	66	3.8	582	2	T06380	beta-fructofuranos	1207	65.5	3.7	434	2	T04248	hypothetical prote
1135	66	3.8	600	2	S56744	mucin (clone pGM7-	1208	65.5	3.7	436	2	T39855	beta-transducin -
1136	66	3.8	622	2	T04141	starch synthase (B	1209	65.5	3.7	456	2	T40416	hypothetical prote
1137	66	3.8	623	2	I64034	hypothetical prote	1210	65.5	3.7	469	1	H84669	acid phosphatase (
1138	66	3.8	652	2	S47979	aliB protein precu	1211	65.5	3.7	482	1	A34671	triacylglycerol li
1139	66	3.8	656	2	AB1479	probable cell surf	1212	65.5	3.7	488	2	T21701	hypothetical prote
1140	66	3.8	661	2	A49901	coat protein gp1 -	1213	65.5	3.7	497	2	H83886	hypothetical prote
1141	66	3.8	686	2	A59348	formate dehydrogen	1214	65.5	3.7	502	2	T20130	hypothetical prote
1142	66	3.8	689	2	S66006	conserved hypothet	1215	65.5	3.7	513	2	S58200	probable membrane
1143	66	3.8	704	2	T13665	NADH2 dehydrogenas	1216	65.5	3.7	521	1	HYBSN	bacillolysin (EC 3
1144	66	3.8	711	2	C87597	alpha-glucuronidas	1217	65.5	3.7	534	1	VCVWSF	env polyprotein -
1145	66	3.8	713	2	D85503	lysine decarboxyla	1218	65.5	3.7	535	2	T47790	hypothetical prote
1146	66	3.8	713	2	D90652	lysine decarboxyla	1219	65.5	3.7	551	2	H86121	trehalase 6-P hydr
1147	66	3.8	713	2	B64743	lysine decarboxyla	1220	65.5	3.7	551	2	H91280	trehalase 6-P hydr
1148	66	3.8	732	2	T44483	receptor-like prot	1221	65.5	3.7	554	2	F90462	sugar-binding per1
1149	66	3.8	741	2	D81798	lactoferrin-bindin	1222	65.5	3.7	584	1	ALBY	alpha-glucosidase
1150	66	3.8	776	2	A55448	Ah receptor nuclea	1223	65.5	3.7	584	2	S46183	alpha-glucosidase
1151	66	3.8	777	2	G69310	penicillin G acyla	1224	65.5	3.7	584	2	S46183	alpha-glucosidase
1152	66	3.8	778	2	A13064	glucose dehydrogen	1225	65.5	3.7	591	2	G96592	probable beta-fruc
1153	66	3.8	778	2	G98221	glucose dehydrogen	1226	65.5	3.7	607	2	H88065	protein Tf6Al.1 [l
1154	66	3.8	779	2	AE2401	alpha-glucosidase	1227	65.5	3.7	608	2	JQ1462	phosphoenolpyruvat
1155	66	3.8	784	2	T13579	hypothetical prote	1228	65.5	3.7	617	2	T15408	hypothetical prote
1156	66	3.8	799	2	T01663	1,4-alpha-glucan b	1229	65.5	3.7	620	1	UYPVAP	noncapsid protein
1157	66	3.8	846	2	A86663	aminopeptidase N [	1230	65.5	3.7	622	2	F71174	hypothetical prote
1158	66	3.8	886	2	A59223	nitrate reductase	1231	65.5	3.7	625	2	T06184	sucrose-fructan 6-
1159	66	3.8	893	2	E95053	cell wall surface	1232	65.5	3.7	627	2	S14683	lg mu chain precu
1160	66	3.8	902	2	A60560	formyltetrahydrofo	1233	65.5	3.7	637	2	T13432	gamma-glutamyltran
1161	66	3.8	912	2	F71433	probable growth re	1234	65.5	3.7	642	1	SYECTT	threonine-tRNA lig
1162	66	3.8	940	2	S49087	lactoferrin bindin	1235	65.5	3.7	642	2	B90932	threonine tRNA syn
1163	66	3.8	958	1	JN0102	glucan 1,4-alpha-g	1236	65.5	3.7	642	2	P85780	threonine tRNA syn
1164	66	3.8	980	2	H90681	probable flagellin	1237	65.5	3.7	642	2	AB0297	threonine-tRNA lig
1165	66	3.8	1024	2	H87599	TonB-dependent rec	1238	65.5	3.7	648	2	S71885	sex-determining pr
1166	66	3.8	1036	2	S73601	protein P200 - Myc	1239	65.5	3.7	652	2	E90505	hypothetical prote
1167	66	3.8	1166	2	T15628	hypothetical prote	1240	65.5	3.7	681	2	E83636	oligopeptidase A P
1168	66	3.8	1180	2	T31066	vascular cadherin-	1241	65.5	3.7	702	2	T12677	NADH2 dehydrogenas
1169	66	3.8	1289	1	GURPT4	proximal tail fibe	1242	65.5	3.7	713	2	AB0531	lysine decarboxyla
1170	66	3.8	1360	2	T39922	hypothetical prote	1243	65.5	3.7	728	1	NR5CA	1,4-alpha-glucan b
1171	66	3.8	1385	2	D89824	hypothetical prote	1244	65.5	3.7	730	2	JH0798	fasciclin IV precu
1172	66	3.8	1426	2	E90456	oxydoreductase, pr	1245	65.5	3.7	759	2	B84538	hypothetical prote
1173	66	3.8	1584	2	T18276	protein-tyrosine k	1246	65.5	3.7	770	2	S60676	cellobiose oxidase
1174	66	3.8	1948	2	B69511	N conserved hypoth	1247	65.5	3.7	782	2	A61625	tenascin-like prot
1175	66	3.8	2185	1	GNNYB3	genome polyprotein	1248	65.5	3.7	790	2	S61587	transcription acti
1176	66	3.8	2204	2	A70524	probable PPE prote	1249	65.5	3.7	792	2	AD0104	probable glucosida
1177	66	3.8	2228	2	T14029	variant-specific s	1250	65.5	3.7	814	2	S19658	microbial collagen
1178	66	3.8	4543	1	A53102	alpha-2-macroglobu	1251	65.5	3.7	815	2	C71810	type I restriction
1179	66	3.8	4544	1	S02392	alpha-2-macroglobu	1252	65.5	3.7	838	2	T20125	hypothetical prote
1180	66	3.8	4545	1	S25111	alpha-2-macroglobu	1253	65.5	3.7	844	2	B83136	probable fibrial
1181	65.5	3.7	189	2	A36846	I2R protein - vari	1254	65.5	3.7	891	2	AB2755	beta-mannosidase p
1182	65.5	3.7	189	2	T28523	hypothetical prote	1255	65.5	3.7	903	2	AB7704	aconitate hydratase
1183	65.5	3.7	189	2	C72161	J2R protein - vari	1256	65.5	3.7	910	2	B83451	aconitate hydratase
1184	65.5	3.7	191	2	G85814	probable outer mem	1257	65.5	3.7	1015	2	T15830	hypothetical prote
1185	65.5	3.7	230	2	I50097	MHC class II beta	1258	65.5	3.7	1020	2	D83679	hypothetical prote
1186	65.5	3.7	245	2	E71948	probable outer mem	1259	65.5	3.7	1041	2	T31437	integrin alpha cha
1187	65.5	3.7	255	2	AC0384	probable exported	1260	65.5	3.7	1054	2	T310933	chitinase (EC 3.2.
1188	65.5	3.7	273	2	T42146	hypothetical prote	1261	65.5	3.7	1072	2	A38457	integrin alpha-6 c
1189	65.5	3.7	279	2	T00225	hypothetical prote	1262	65.5	3.7	1078	2	F97907	hyaluronate lyase
1190	65.5	3.7	293	2	JQ0380	proteinase T (EC 3	1263	65.5	3.7	1097	2	T40678	hypothetical prote
1191	65.5	3.7	311	2	G86324	hypothetical prote	1264	65.5	3.7	1157	2	F97255	fusion of alpha-gl
1192	65.5	3.7	326	2	S26216	glutamate-ammonia	1265	65.5	3.7	1177	2	A36984	protein-tyrosine k
1193	65.5	3.7	327	2	D82678	transcription regu	1266	65.5	3.7	1345	2	S55669	segment protein 7
1194	65.5	3.7	338	2	S65535	light-harvesting c	1267	65.5	3.7	1567	2	S11672	ice nucleation pro
1195	65.5	3.7	341	2	JQ1189	CbHc protein - Cox	1268	65.5	3.7	1609	2	T01797	hypothetical prote
1196	65.5	3.7	357	2	T20659	hypothetical prote	1269	65.5	3.7	1627	2	S65464	pregnancy-associat
1197	65.5	3.7	359	1	A31425	uracil-DNA glycosy	1270	65.5	3.7	1657	2	T25421	hypothetical prote



1271	65.5	3.7	1778	2	T50074	probable nucleopor	1344	65	3.7	749	2	A45887	outer capsid prote
1272	65.5	3.7	1939	2	D97316	probable S-layer p	1345	65	3.7	760	2	D69865	conserved hypotet
1273	65.5	3.7	2232	2	T34434	hypothetical prote	1346	65	3.7	763	2	S23457	polysulfide reduct
1274	65.5	3.7	2343	2	T31687	surface antigen - P	1347	65	3.7	773	2	JE0387	exo-alpha-sialidas
1275	65	3.7	121	2	A49590	Ig heavy chain V r	1348	65	3.7	791	2	A56241	aryl hydrocarbon r
1276	65	3.7	133	2	C33548	Ig heavy chain V-1	1349	65	3.7	800	2	AD3129	conserved hypotet
1277	65	3.7	144	2	AB3029	hypothetical prote	1350	65	3.7	815	2	E98158	hypothetical prote
1278	65	3.7	191	2	G65017	hypothetical prote	1351	65	3.7	837	2	S38713	CCR4 protein - Yea
1279	65	3.7	226	2	T46058	porin-like protein	1352	65	3.7	838	2	H82939	conserved hypotet
1280	65	3.7	247	1	QBEEF1	HMG3 protein prec	1353	65	3.7	875	2	T12794	hypothetical yong
1281	65	3.7	254	1	HLHDD7	MHC class II histo	1354	65	3.7	878	2	S74207	lipoxigenase (EC 1
1282	65	3.7	258	2	T10083	expansin S2 precu	1355	65	3.7	879	2	D66804	unknown protein T5
1283	65	3.7	280	2	T29200	hypothetical prote	1356	65	3.7	904	2	AH2019	hypothetical prote
1284	65	3.7	285	2	S74771	hypothetical prote	1357	65	3.7	905	1	A27410	nucleotide diphosp
1285	65	3.7	294	2	S49152	nucleoside-specifi	1358	65	3.7	907	2	T48500	Mei2-like protein
1286	65	3.7	296	2	T16693	peroxidase (EC 1.1	1359	65	3.7	932	2	A80003	DNA-directed DNA p
1287	65	3.7	320	2	T16823	hypothetical prote	1360	65	3.7	966	2	H97717	hypothetical prote
1288	65	3.7	322	2	T03686	peroxidase (EC 1.1	1361	65	3.7	995	2	S75712	protein C05D1.1 l
1289	65	3.7	324	2	A39889	peroxidase (EC 1.1	1362	65	3.7	1070	2	A88483	cellulase (EC 3.2.
1290	65	3.7	342	2	S14432	heterogeneous ribo	1363	65	3.7	1104	2	A60999	alpha-amylase (EC
1291	65	3.7	342	2	H86300	probable glutamate	1364	65	3.7	1136	2	T30878	dynamin heavy chain
1292	65	3.7	342	2	B96021	Flk19.12 protein	1365	65	3.7	1148	2	T18770	probable calcium c
1293	65	3.7	363	2	S30386	mannan endo-1,4-be	1366	65	3.7	1172	1	TSHUP2	thrombospondin 2 p
1294	65	3.7	370	2	T48578	hypothetical prote	1367	65	3.7	1301	1	A41622	protein-tyrosine-p
1295	65	3.7	373	2	C81689	tRNA (5-methylamin	1368	65	3.7	1367	1	IGHUR1	insulin-like growt
1296	65	3.7	376	2	E84742	hypothetical prote	1369	65	3.7	1398	2	H50698	Rhd core protein
1297	65	3.7	380	1	TVFVMM	hypothetical prote	1370	65	3.7	1398	2	H50698	hypothetical prote
1298	65	3.7	384	2	T37232	protein kinase (EC	1371	65	3.7	1400	2	E90886	Rhes core protein
1299	65	3.7	389	2	B42708	secreted beta-mann	1372	65	3.7	1445	1	A48148	protein-tyrosine-p
1300	65	3.7	390	2	T14794	serine-type D-Ala-	1373	65	3.7	2083	2	T42721	CRP-ductin-alpha p
1301	65	3.7	400	2	T19517	hypothetical prote	1374	65	3.7	2098	2	T18397	protein CTRP - mal
1302	65	3.7	400	2	AH2303	hypothetical prote	1375	65	3.7	2130	2	AB0821	probable exported
1303	65	3.7	404	2	H65128	hypothetical prote	1376	65	3.7	2248	2	A35938	profilaggrin - hum
1304	65	3.7	404	2	E91287	hypothetical prote	1377	65	3.7	2366	2	S10317	toxigen B - Clostrid
1305	65	3.7	415	2	T44436	3-oxoacyl-[acyl-ca	1378	65	3.7	2616	2	A57096	nudel protein prec
1306	65	3.7	416	2	T02194	glutamate-pectinase	1379	65	3.7	2681	2	T34513	hypothetical prote
1307	65	3.7	429	1	AJFBDQ	glutamate-ammonia	1380	65	3.7	273	2	AC1483	hypothetical prote
1308	65	3.7	451	2	JE0313	exoglucanase (EC 3	1381	64.5	3.7	274	2	T30588	gp330 protein prec
1309	65	3.7	455	2	F64617	hypothetical prote	1382	64.5	3.7	280	2	JC7852	14K protein - narc
1310	65	3.7	457	2	S63608	glutamate dehydrog	1383	64.5	3.7	297	1	S70988	hypothetical prote
1311	65	3.7	480	2	AB0148	catalase (EC 1.11.	1384	64.5	3.7	302	2	T02617	reg I, regeneratin
1312	65	3.7	487	2	D95887	probable aldehyde-	1385	64.5	3.7	323	2	T09873	ribonuclease (EC 3
1313	65	3.7	502	2	A70582	hypothetical prote	1386	64.5	3.7	324	2	C41335	stylar glycoprotei
1314	65	3.7	507	2	A40659	elastase (EC 3.4.2	1387	64.5	3.7	326	1	D64560	outer membrane pro
1315	65	3.7	519	2	F64163	hypothetical prote	1388	64.5	3.7	326	2	B72278	opacity protein P.
1316	65	3.7	523	2	B95922	hypothetical nucle	1389	64.5	3.7	329	1	AJZJQ2	B. subtilis IolB p
1317	65	3.7	523	2	C97228	probable peptide A	1390	64.5	3.7	330	2	D96787	hypothetical prote
1318	65	3.7	547	2	T29567	hypothetical prote	1391	64.5	3.7	331	2	A96621	chitosanase (EC 3.
1319	65	3.7	588	2	S30929	catechol oxidase (	1392	64.5	3.7	342	2	T18819	gnd protein - Myco
1320	65	3.7	591	2	B83457	glyoxylate carboli	1393	64.5	3.7	358	2	S15908	hypothetical prote
1321	65	3.7	595	2	A35847	Fos-related antige	1400	64.5	3.7	359	2	F89075	probable cellulase
1322	65	3.7	599	2	UN0818	transferrin-bindin	1401	64.5	3.7	365	1	MMECNC	microbial serine p
1323	65	3.7	601	2	T11677	probable transcrip	1402	64.5	3.7	382	2	T27076	conserved hypotet
1324	65	3.7	614	1	QRECBT	vitamin B12 recept	1403	64.5	3.7	382	2	T08088	glutamate-ammonia
1325	65	3.7	624	2	G82508	hypothetical prote	1404	64.5	3.7	391	2	A13375	outer membrane por
1326	65	3.7	634	2	T41319	conserved hypotet	1405	64.5	3.7	392	2	A75503	hypothetical prote
1327	65	3.7	639	2	S23118	proprotein convert	1406	64.5	3.7	397	2	AE3303	hypothetical prote
1328	65	3.7	640	2	S23008	insulin-like growt	1407	64.5	3.7	407	2	T21956	hypothetical prote
1329	65	3.7	650	2	T06648	hypothetical prote	1408	64.5	3.7	409	2	P83899	hypothetical prote
1330	65	3.7	652	2	G95177	hypothetical prote	1409	64.5	3.7	414	2	T44513	hypothetical prote
1331	65	3.7	652	2	E98044	hypothetical prote	1410	64.5	3.7	416	2	G72305	glutamate dehydrog
1332	65	3.7	654	2	F83376	probable N-glycosyl	1411	64.5	3.7	421	2	S10514	glutamate dehydrog
1333	65	3.7	664	2	F83376	conserved hypotet	1412	64.5	3.7	421	2	G95308	alpha-amylase (EC
1334	65	3.7	667	2	T33526	hypothetical prote	1413	64.5	3.7	427	1	KGHUL1	probable ABC sugar
1335	65	3.7	668	2	E71879	probable outer mem	1414	64.5	3.7	427	1	KGHUL1	kininogen, LMW pre
1336	65	3.7	678	2	T05821	hypothetical prote	1415	64.5	3.7				
1337	65	3.7	681	2	T33381	hypothetical prote	1416	64.5	3.7				
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1341	65	3.7	702	2	AD0625	NADH2 dehydrogenas							
1342	65	3.7	705	2	T00975	conserved hypotet							
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						DEF (CIA1) protein							

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 1498 64 3.7 366 2 D90888  
 1499 64 3.7 376 2 S47986  
 1500 64 3.7 376 2 S24408

ALIGNMENTS

RESULT 1

JE0328  
 Intelectin - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C:Accession: JE0328  
 R:Komiyama, T.; Tanigawa, Y.; Hirohashi, S.  
 Biochem. Biophys. Res. Commun. 251, 759-762, 1998  
 A:Title: Cloning of the novel gene intelectin, which is expressed in intestinal paneth  
 A:Reference number: JE0328; MUID:99008898; PMID:9790983  
 A:Accession: JE0328  
 A>Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-313 <KOM>  
 A:Cross-references: UNIPROT:O88310; UNIPARC:UPI000029628; DDBJ:AB016496; NID:G3357908;

Query Match 81.7%; Score 1427; DB 2; Length 313;

Best Local Similarity 81.5%; Pred. No. 5.6e-106; Mismatches 35; Indels 0; Gaps 0;

Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

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 DB 1 MTQLGFLLFIMVATGCSAAEENLDTNRWNSFFSLPRSCKEIKQHTKAQDGLYFLRT 60  
 QY 61 ENGVIYQFCDMTSGGGWTLVASVHENDMRGKCTVGRWSSQQSKADYPGSGDNWANY 120  
 DB 61 KNGVIYQFCDMTSGGGWTLVASVHENDMRGKCTVGRWSSQQSKADYPGSGDNWANY 120  
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 DB 121 NTFGSAAEATSDDYKNPGYDIOAKDLGIWHVPNKSPLHNRKSSLLRYTDTGFIOTIG 180  
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 QY 241 FNNERAAALCAGMRVTCNTEHHICGGGYPPEASQCGDFSGDFMSGYGTHVGYSSS 300  
 DB 241 FNNERAAALCAGMRVTCNTEHHICGGGYPPEASQCGDFSGDFMSGYGTHVGYSSS 300  
 QY 301 REITEAVALLPFR 313  
 DB 301 RKITEAVALLPFR 313

RESULT 2

S49589  
 cortical granule lectin - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 05-Mar-1995 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004  
 C:Accession: S49589  
 R:Chang, B.Y.; Wardrip, N.J.; Hedrick, J.L.  
 submitted to the EMBL Data Library, November 1994  
 A:Description: Molecular cloning and characterization of cortical granule lectin: an es  
 A:Reference number: S49589  
 A:Accession: S49589  
 A>Status: preliminary









J. Biol. Chem. 268, 12812-12817, 1993  
 A>Title: Topological analysis of quinoprotein glucose dehydrogenase in Escherichia coli  
 A;Reference number: A45997; MUID:93286127; PMID:8509415  
 A;Accession: A45997  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <YAM>  
 A;Cross-references: UNIPARC:UPI0000171FB2  
 R;Fujiita, N.  
 submitted to the EMBL Data Library, January 1994  
 A;Reference number: S45201  
 A;Accession: S45201  
 A;Molecule type: DNA  
 A;Residues: 1-796 <FUJ>  
 A;Cross-references: UNIPARC:UPI0000129320; EMBL:D26562; NID:G473770; PIDN:BAA05580.1; PID:  
 R;Yamada, M.; Asaka, S.; Saito, M.H.; Yamada, Y.  
 J. Bacteriol. 175, 568-571, 1993  
 A>Title: Characterization of the gcd gene from Escherichia coli K-12 W3110 and regulation  
 A;Reference number: I41228; MUID:93123180; PMID:8419307  
 A;Accession: I41228  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-148, 'H', 150, 'KRRCHT', 157-192, 'K', 194-665, 'H', 667-796 <RES>  
 A;Cross-references: UNIPARC:UPI000016F19A; GB:D12651; NID:G216555; PIDN:BAA02174.1; PID:  
 C;Genetics:  
 A;Gene: gcd  
 A;Map position: 3 min  
 A;Function:  
 A;Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone  
 A;Pathway: respiratory chain  
 C;Superfamily: glucose/Alcohol /Shikimate dehydrogenase  
 F;Keywords: oxidoreductase; pyruvate dehydrogenase; respiratory chain; transmembrane p  
 F;11-37/Domain: transmembrane #status predicted <TM1>  
 F;41-59/Domain: transmembrane #status predicted <TM2>  
 F;63-81/Domain: transmembrane #status predicted <TM3>  
 F;96-110/Domain: transmembrane #status predicted <TM4>  
 F;120-140/Domain: transmembrane #status predicted <TM4>  
 F;93.95/Binding site: ubiquinone (Arg, Asp) #status predicted <TM5>  
 F;466/Active site: Asp #status predicted

Query Match 5.7%; Score 99; DB 1; Length 796;  
 Best Local Similarity 22.3%; Pred. No. 4.8;  
 Matches 90; Conservative 44; Mismatches 133; Indels 136; Gaps 24;  
 QY 8 LFLIATTRG---WSTD---EANTYFKETWC-----SSPSLPRSCKEIKDECPS 50  
 Db 236 LFALDAASGKEKWHYDELKTNESFOHVTGCRGVSYHEAKAETASP-----EVMADCFR 288  
 QY 51 AF-----DG-LYFLRTENGVIYQTCDMTSGGGWTLVASVHEND----- 89  
 Db 289 RIILPVNDGRLIAINAENGLKLCETPANK-----GVLNLSNMPDTKPGLYEPTSPPIITDK 344  
 QY 90 ---MRGKCTVGRWSQOQSKA-----DYPEGDNWANTYTFGSABAATSDDYK----- 135  
 Db 345 TIWAGSVT--DNFSTRETSVGIRGVDVNTGELLWAFDPGAKDPNAIPSDRHTFTFNSPN 402  
 QY 136 --NPGYDIQAKDLGIWHVP-----NKSPMQHWRNSSLRYRTDTGFL-----QT 178  
 Db 403 SWAPAAAYDAK--LDLVLPMGVTPPDWGNRTPEQERYASSILALNATTGLAWSYQT 459  
 QY 179 LGHNLFGI-----YQKPVYKGEKCTWDN-----GPIVPPV 210  
 Db 460 VHHDLWMDLPAQPTLADITVNGQKVPVIYAPAK--TGNIFVLDRRNGELVWPAPEKVP 517  
 QY 211 YDFGDAQKTASYSPYQOREFTAGF--VOFRVFNERRAANALCAGM--RVTCNTEHHCIG 267  
 Db 518 Q--GAAK--GDYVTP-----TOPFSELSFRPTKDLGDMWGATMFDQLVCRVMFQMR 567  
 QY 268 GGGYPPEASPOQC-----GDFSGPWSGVTHGVSSSREITEA 306  
 Db 568 YEGIFTPPSEQTLVFPNGLMFEWGG-----ISVDPNREVAIA 606

## RESULT 13

H90644

Glucose dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509)  
 C;Species: Escherichia coli  
 C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
 C;Accession: H90644  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehi, K.; Yokoyama, K.; Han, C.G.  
 Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
 DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A;Reference number: A99629; MUID:21156231; PMID:11258796  
 A;Accession: H90644  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-796 <HAY>  
 A;Cross-references: UNIPARC:UPI00000D0879; GB:BA000007; PIDN:BA033551.1;  
 A;Experimental source: strain O157:H7, substrain RIMD 0509952  
 C;Genetics:

## RESULT 12

H85495

Glucose dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C;Species: Escherichia coli  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
 C;Accession: H85495  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, J.D.; Mayh  
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamouais, K.; Apodac  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A;Reference number: A85480; MUID:21074935; PMID:11206551  
 A;Accession: H85495  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-796 <STO>  
 A;Cross-references: UNIPARC:O8X946; UNIPARC:UPI00000D0879; GB:AE005174; NID:G12512839;  
 A;Experimental source: strain O157:H7, substrain EDL933  
 C;Genetics:  
 A;Gene: gcd  
 C;Superfamily: glucose/Alcohol /Shikimate dehydrogenase

Query Match 5.7%; Score 99; DB 2; Length 796;

Best Local Similarity 22.3%; Pred. No. 4.8;

Matches 90; Conservative 44; Mismatches 133; Indels 136; Gaps 24;

QY 8 LFLIATTRG---WSTD---EANTYFKETWC-----SSPSLPRSCKEIKDECPS 50

Db 236 LFALDAASGKEKWHYDELKTNESFOHVTGCRGVSYHEAKAETASP-----EVMADCFR 288

QY 51 AF-----DG-LYFLRTENGVIYQTCDMTSGGGWTLVASVHEND----- 89

Db 289 RIILPVNDGRLIAINAENGLKLCETPANK-----GVLNLSNMPDTKPGLYEPTSPPIITDK 344

QY 90 ---MRGKCTVGRWSQOQSKA-----DYPEGDNWANTYTFGSABAATSDDYK----- 135

Db 345 TIWAGSVT--DNFSTRETSVGIRGVDVNTGELLWAFDPGAKDPNAIPSDRHTFTFNSPN 402

QY 136 --NPGYDIQAKDLGIWHVP-----NKSPMQHWRNSSLRYRTDTGFL-----QT 178

Db 403 SWAPAAAYDAK--LDLVLPMGVTPPDWGNRTPEQERYASSILALNATTGLAWSYQT 459

QY 179 LGHNLFGI-----YQKPVYKGEKCTWDN-----GPIVPPV 210

Db 460 VHHDLWMDLPAQPTLADITVNGQKVPVIYAPAK--TGNIFVLDRRNGELVWPAPEKVP 517

QY 211 YDFGDAQKTASYSPYQOREFTAGF--VOFRVFNERRAANALCAGM--RVTCNTEHHCIG 267

Db 518 Q--GAAK--GDYVTP-----TOPFSELSFRPTKDLGDMWGATMFDQLVCRVMFQMR 567

QY 268 GGGYPPEASPOQC-----GDFSGPWSGVTHGVSSSREITEA 306

Db 568 YEGIFTPPSEQTLVFPNGLMFEWGG-----ISVDPNREVAIA 606





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